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Roberts et al.

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(54) **CLONING, OVEREXPRESSION AND THERAPEUTIC USE OF BIOACTIVE HISTIDINE AMMONIA LYASE**

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(65) **Prior Publication Data**

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Related U.S. Application Data

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(51) **Int. Cl.**⁷ **A61K 38/51**; C12N 9/88

(52) **U.S. Cl.** **424/94.5**; 435/232

(58) **Field of Search** 435/232, 188; 424/94.5

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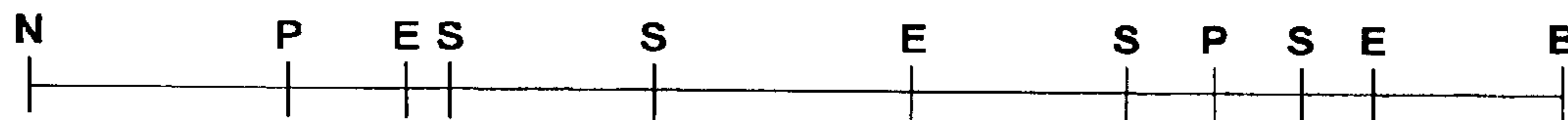
(57) **ABSTRACT**

Histidine ammonia lyase (HAL) isolated from *Corynebacteriaceae* can decrease serum histidine levels, induce accumulation of urocanic acid, and is not inhibited by L-histidinol. As a result, histidine ammonia lyases similar to the one isolated from *Corynebacteriaceae* are uniquely suitable for combination therapy with L-histidinol to treat histidine- and/or histamine-dependent pathologies, for example, infectious viruses, such as human Respiratory Syncytial Virus (RSV), Herpes Simplex Virus (HSV), and Human Immunodeficiency Virus (HIV), as well as cancers.

21 Claims, 26 Drawing Sheets

Restriction pattern of the HAL coding region cut with selected enzymes.

HAL



N - NdeI site introduced at the N-terminus

B - BamHI site introduced at the C-terminus

E - EagI

P - PstI

S - SphI

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Figure 1: Restriction pattern of the HAL coding region cut with selected enzymes.

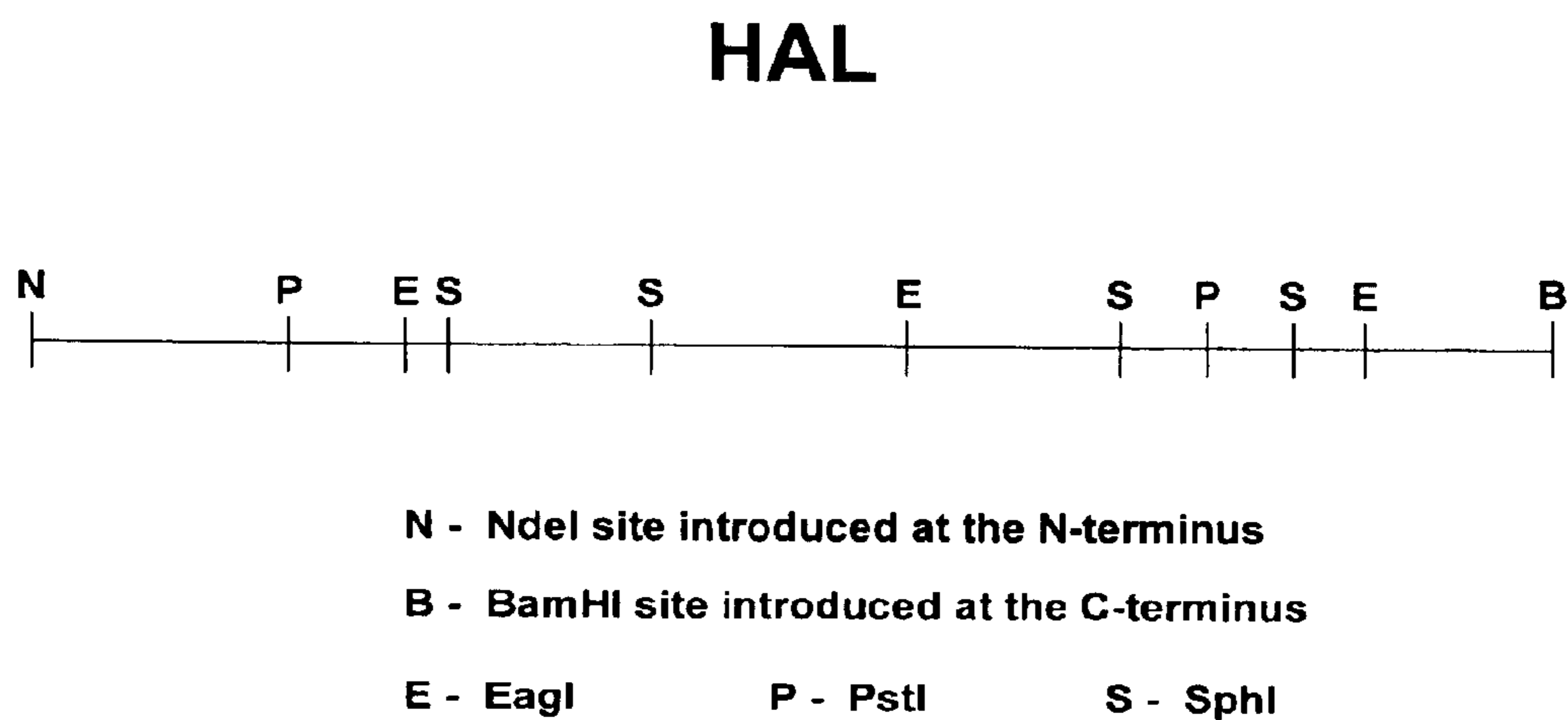


Figure 2: Experimentally derived peptide sequences of HAL

N-terminal

(M)ASAPQITLGLSGATAD

Internal

(M)ALADLDELLDEA

(M)GEPVEREVLRA

Figure 3: SphI digestion pattern of HAL gene showing oligonucleotide and subclones.

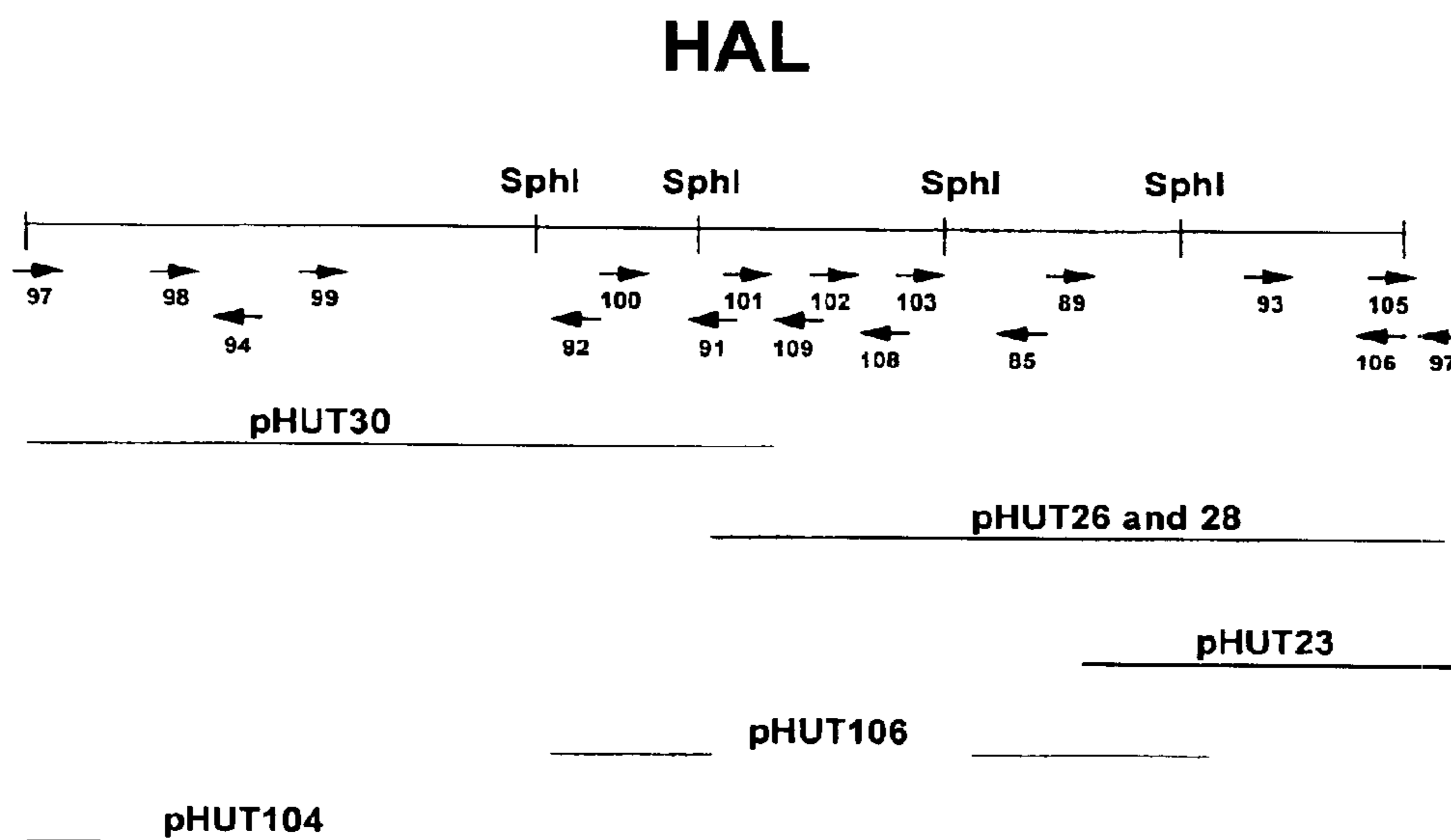


Figure 4: Histidine ammonia lyase overexpressing plasmid.

pHUT102

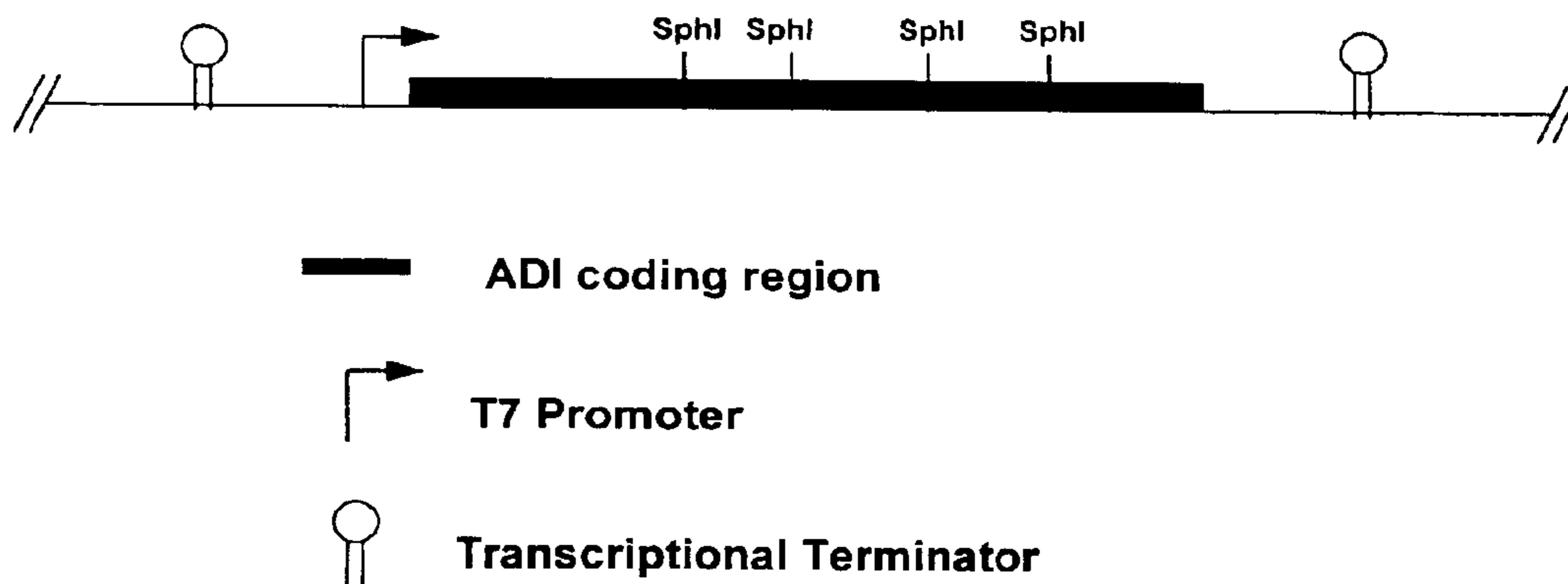


Figure 5: SDS-PAGE showing expression of HAL in *E. coli*.

Lanes: 1 2 3 4

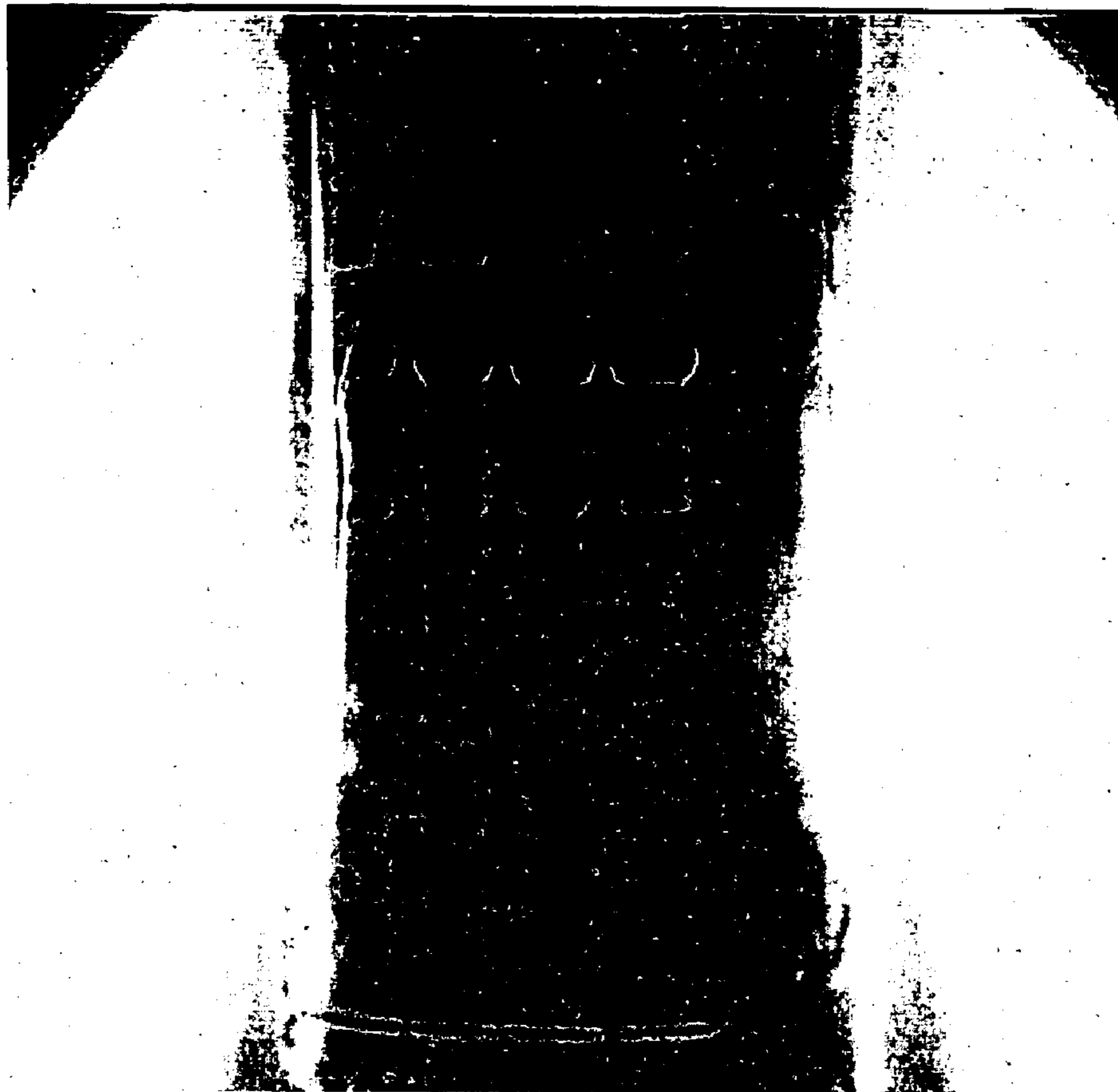


Figure 6: SDS-PAGE showing purification of HAL from *E. coli*

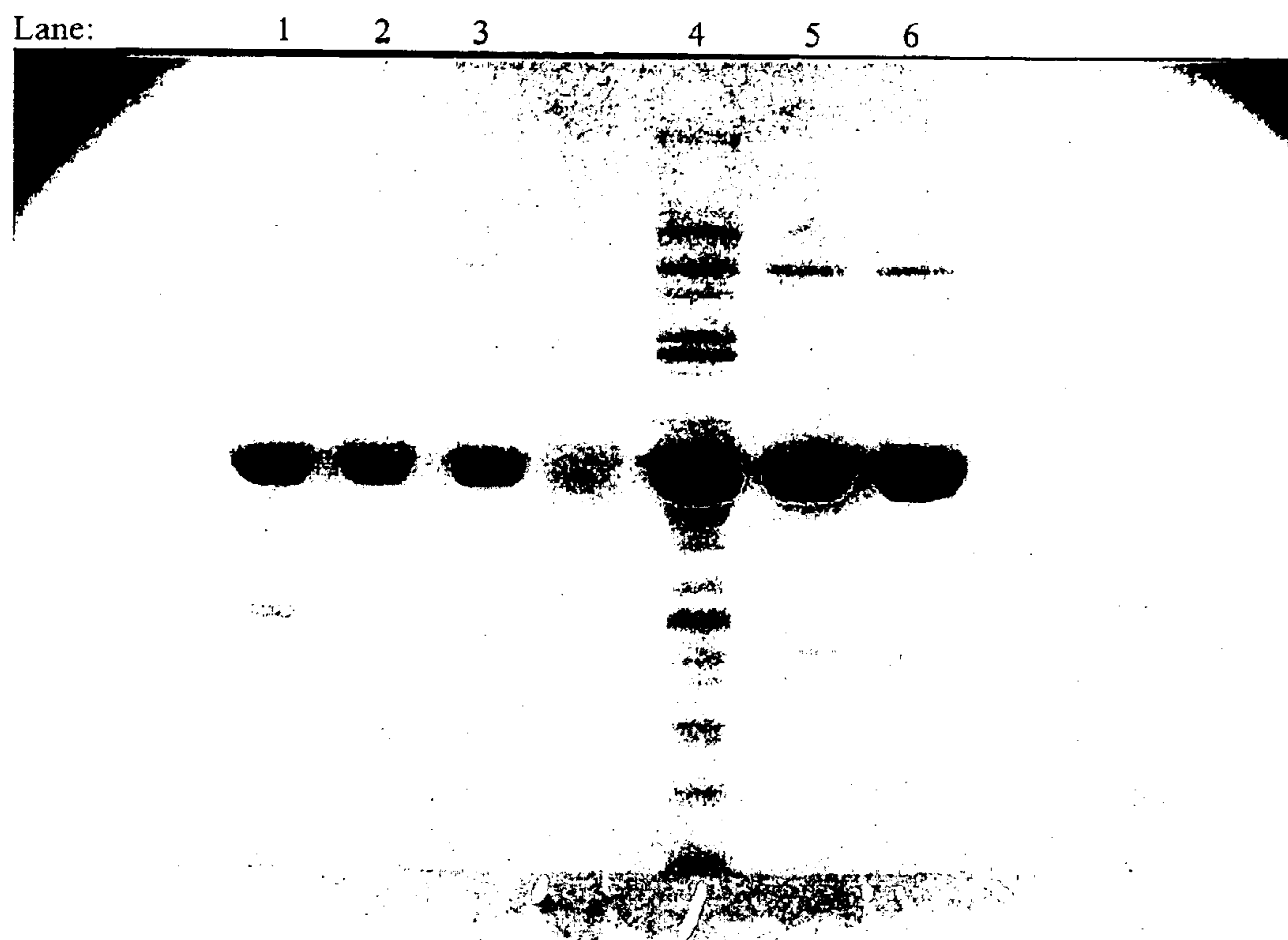


Figure 7: Effect of Temperature on HAL

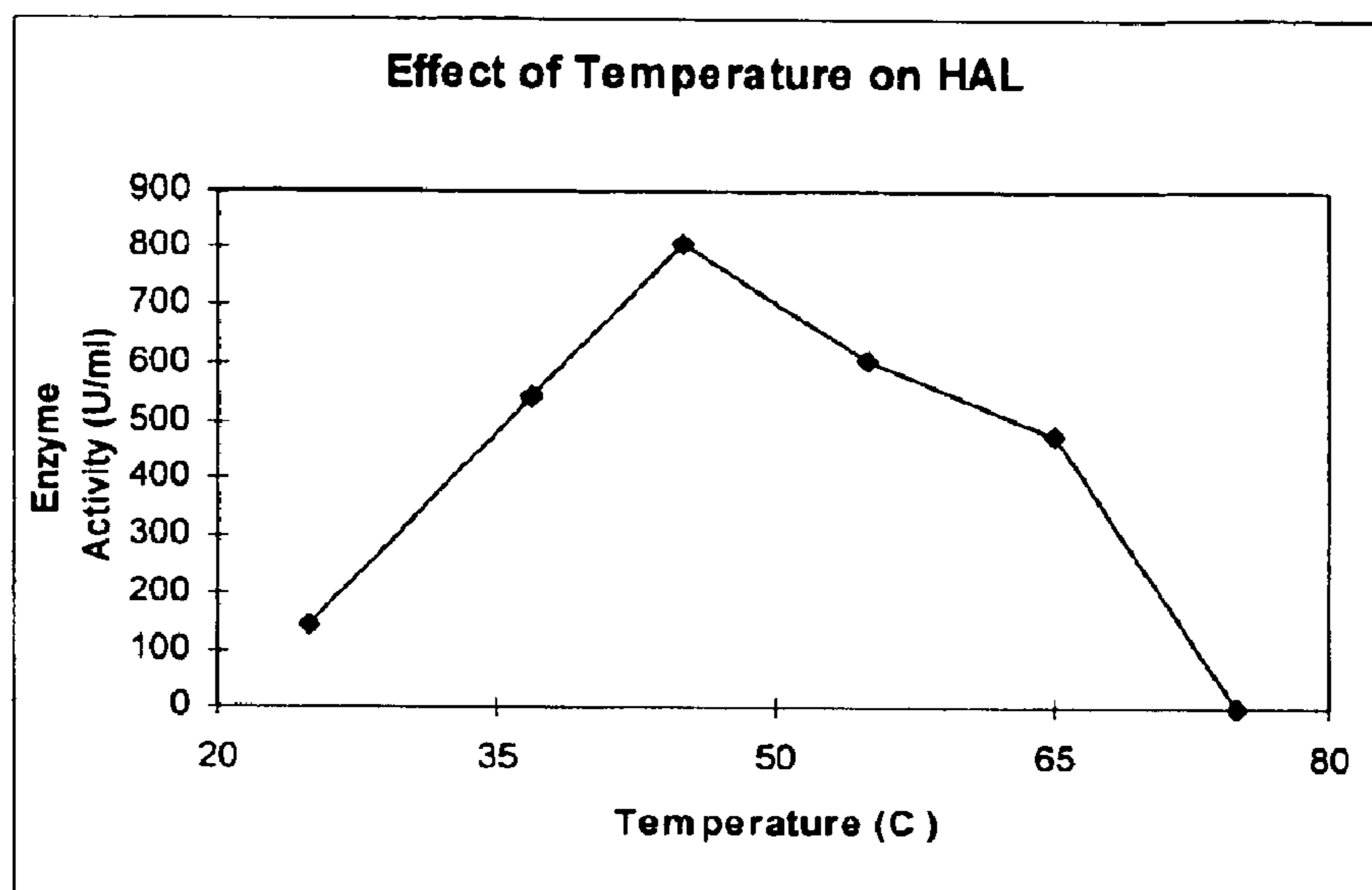


Figure 8: Effect of pH on HAL.

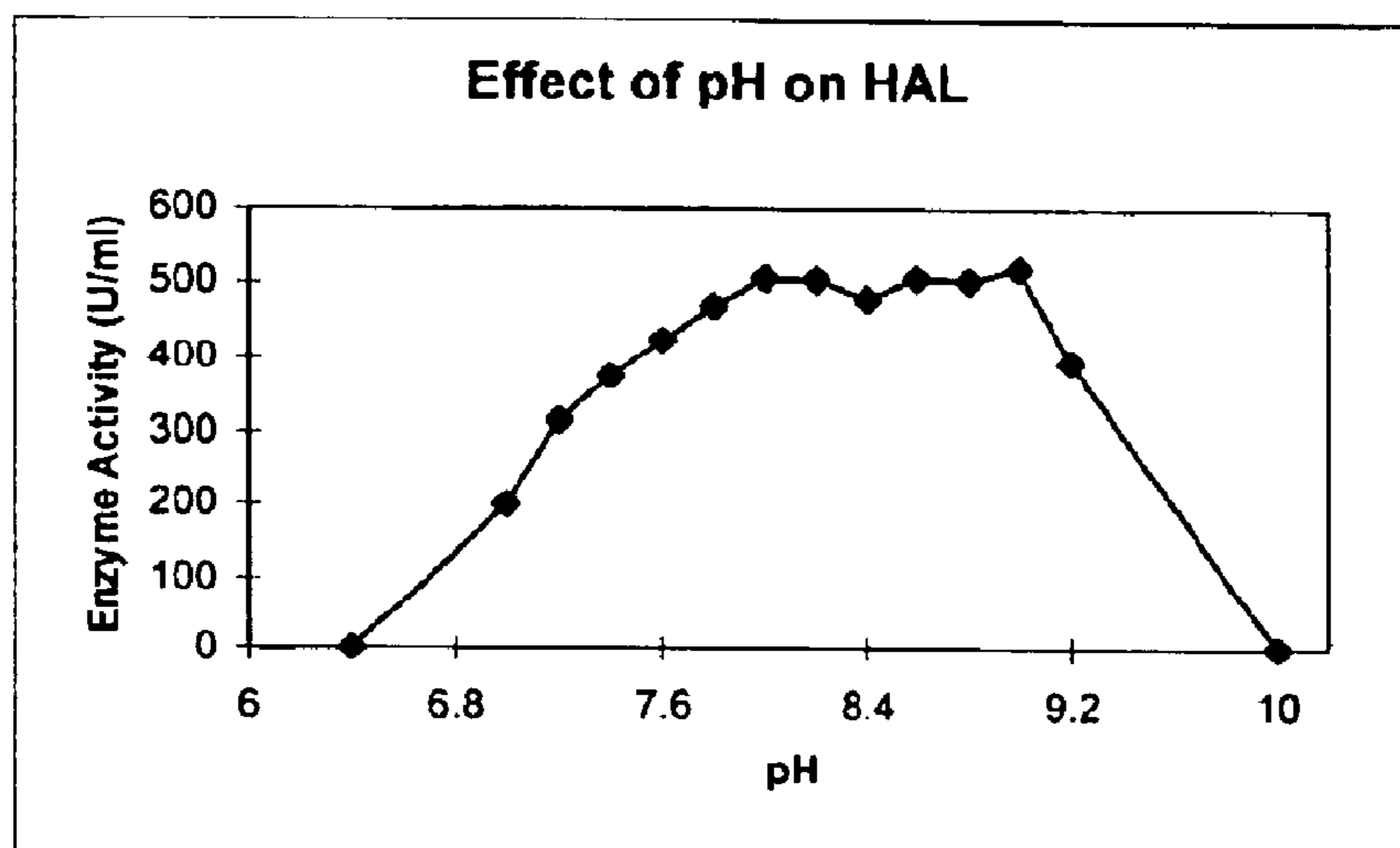


Figure 9: Effect of HAL and Histidinol on HSV.

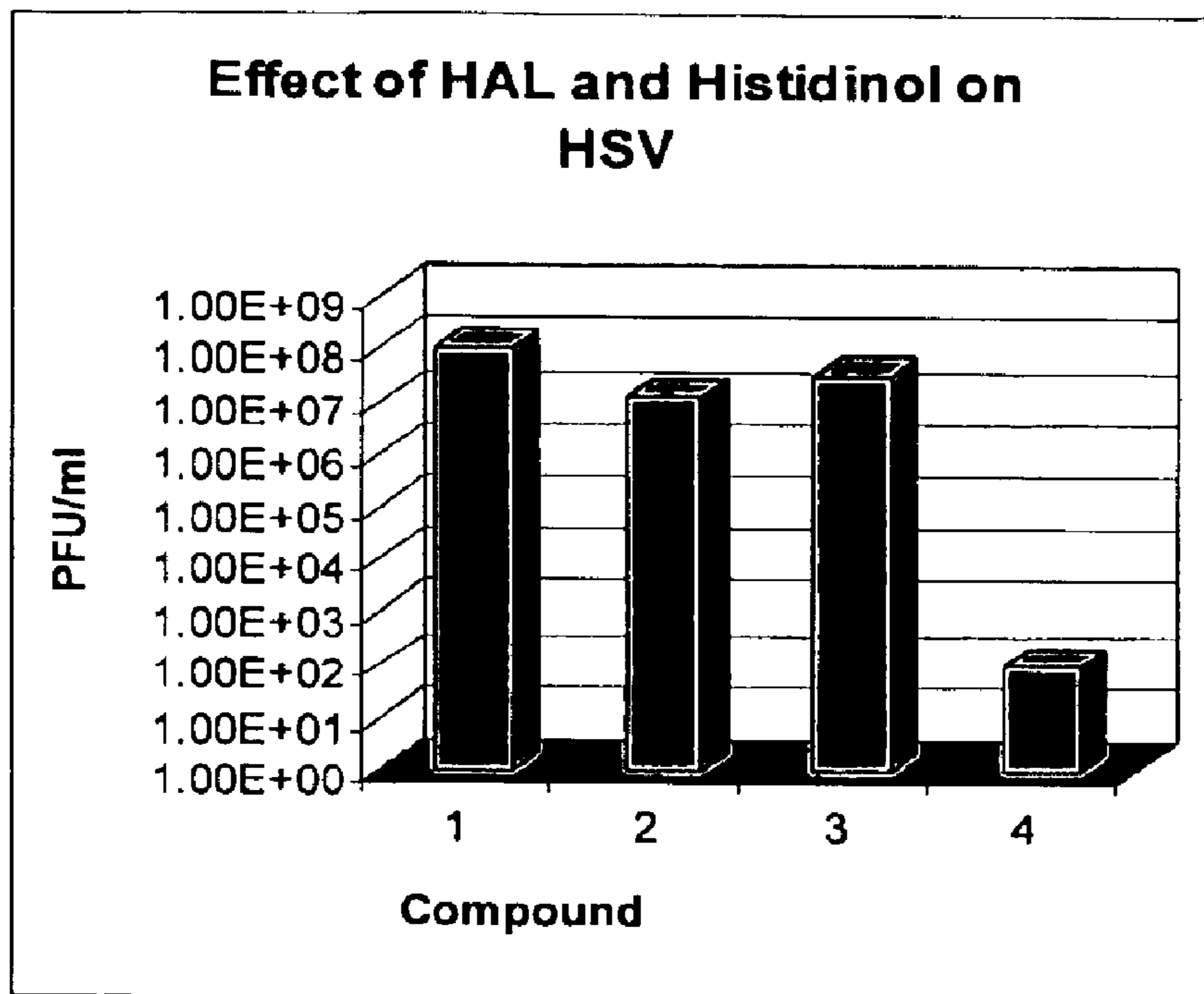


Figure 10: Effectiveness of L-histidinol as a Single Agent

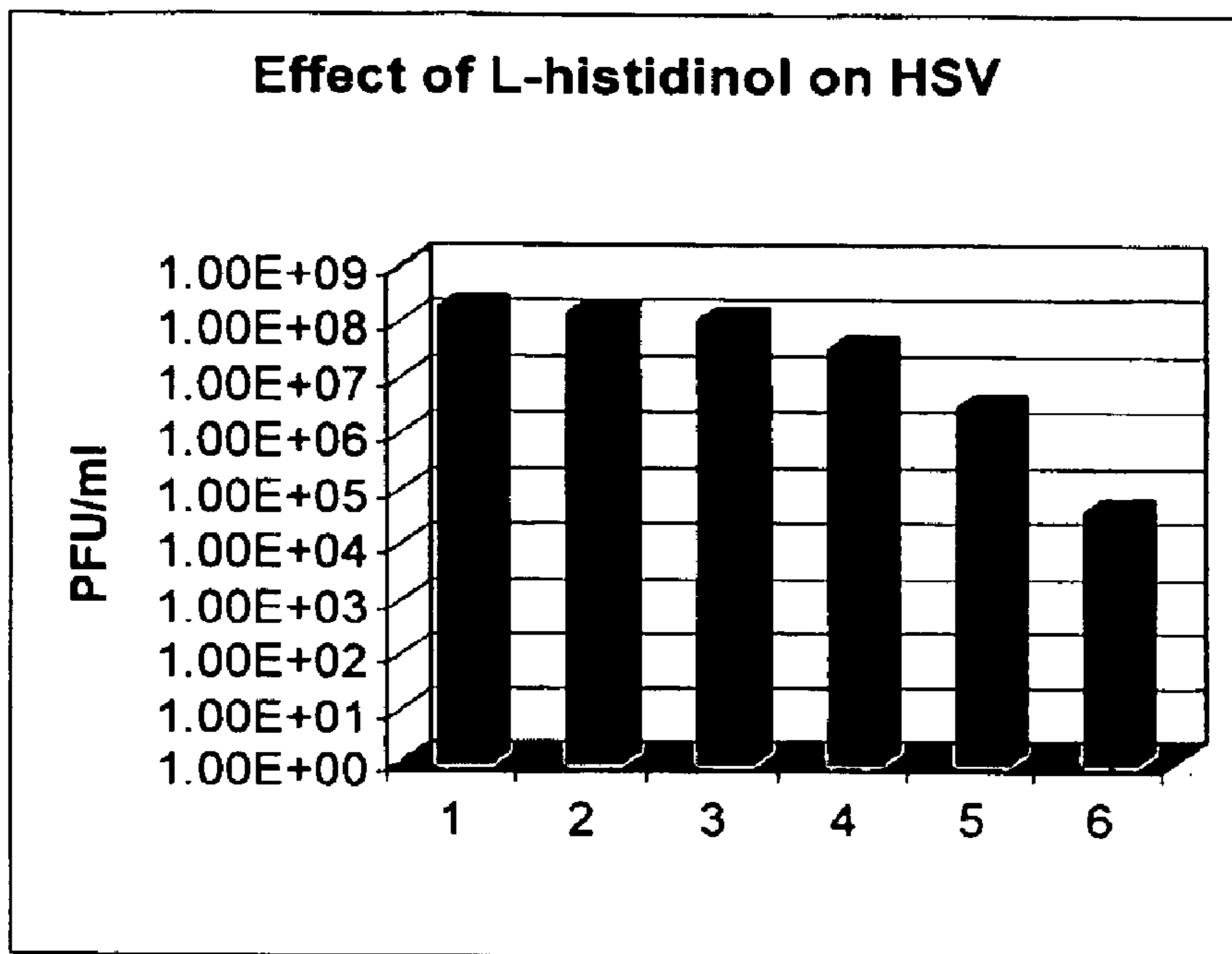


Figure 11: Effect of HAL and Histidinol on RSV.

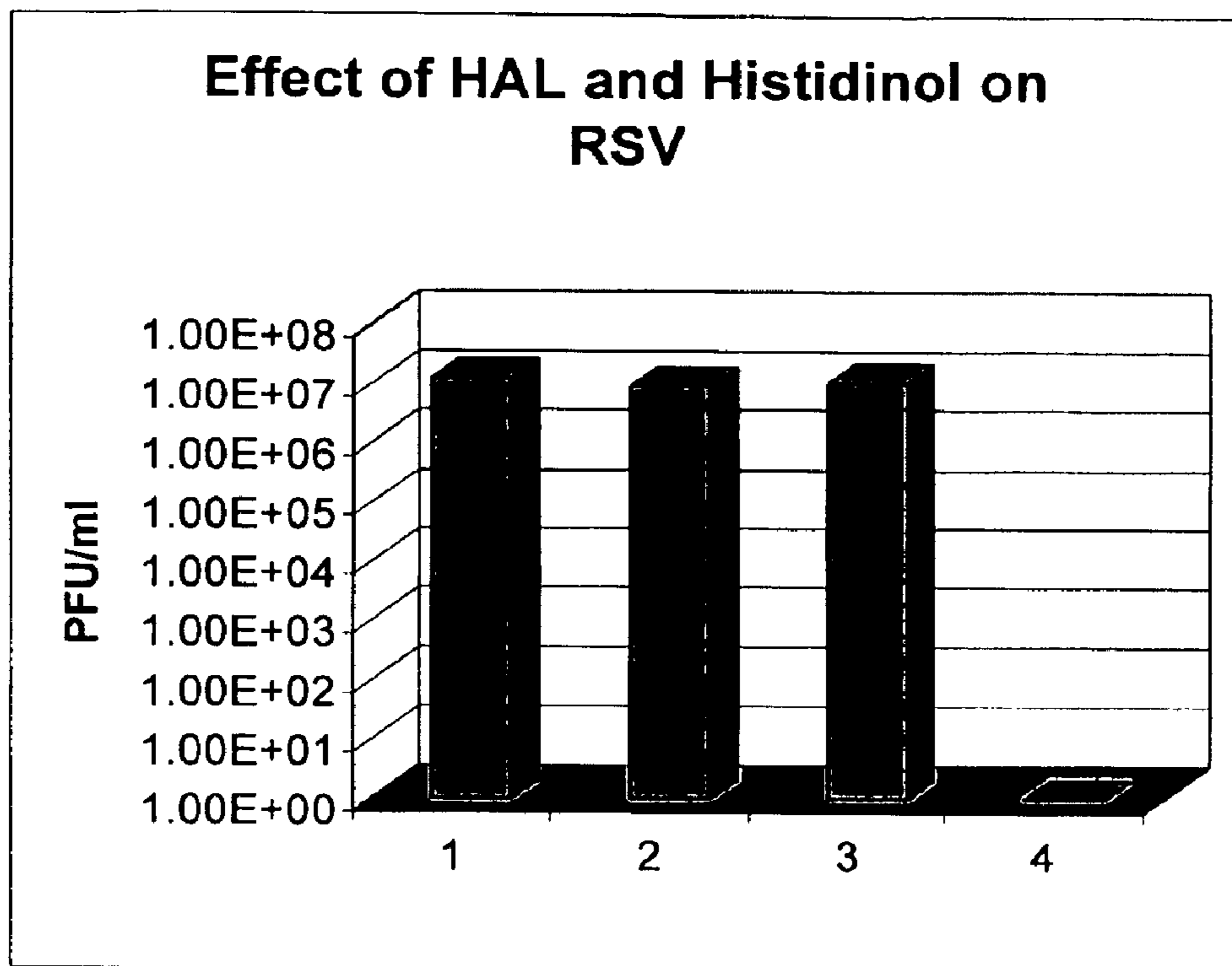


Figure 12: Effect of HAL on RMuLV.

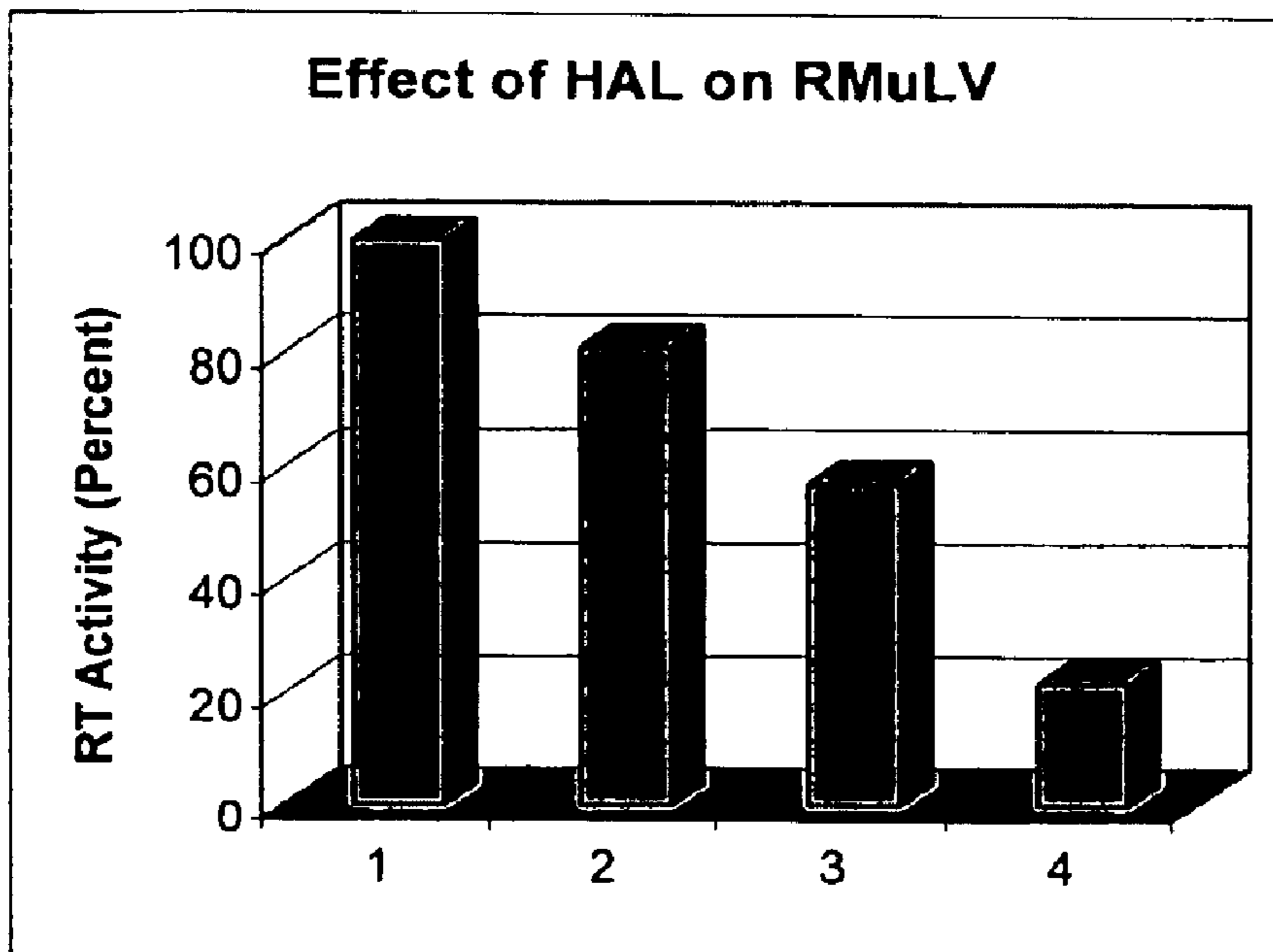


Figure 13A

```

HUTH_PSEPU -----
-
HUTH_RHIME -----
-
HUTH_MOUSE
MPRYTVHVRGEWLAVPCQDGKLTVGWLGREAVRRYMKNKPDNGGFTSVDEVQFLVHRCKG
HUTH_RAT
MPRYTVHVRGEWLAVPCQDGKLSVGWLGREAVRRYMKNKPDNGGFTSVDEVRFVLRCKG
HUTH_HUMAN
MPRYTVHVRGEWLAVPCQDAQLTVGWLGREAVRRYIKNKPDNGGFTSVDDAHFLVRRCKG
HUTH_CAEEL -MRLQVQIGTECVVVPCKP-DDTIHAVAKKSVEKLRRLRPK----
LPLADDYFEVRRTVG
HUTH_BACS -----
-
HUTH_STRGR -----
-
HUTH_CORY -----
-

HUTH_PSEPU -----
-
HUTH_RHIME -----
-
HUTH_MOUSE LGLLDNEDELEVALEDNEFVEVVIEGDVMS-----PDFIPSQPEGVFLYSKYR---
-
HUTH_RAT LGLLDNEDLLEVALEDNEFVEVVIEGDVMS-----PDFIPSQPEGVFLYSKYR---
-
HUTH_HUMAN LGLLDNEDRLEVALENNEFVEVVIEGDAMS-----PDFIPSQPEGVYLYSKYR---
-
HUTH_CAEEL
NSLLDPEDLVSDVLKDSDFIIVAASVEETEDAKEAKKQEEIDNARAEIEKIDNRRRKVSF
HUTH_BACS -----
-
HUTH_STRGR -----
-
HUTH_CORY -----
-

HUTH_PSEPU -----
TELTLPKPGTLTLAQLRAIHAAPVRLQLDASAAPIDASVACVEQIIA
HUTH_RHIME -----
MTVILRPGSVPLSDLETIYWTGAPARLDAAFDAGIAKAAARIAEIVA
HUTH_MOUSE -----
EPEKYIALDGDLSLSTEDLVNLGKGGRYKIKLTSIAEKKVQQSREVIDSIIK
HUTH_RAT -----
EPEKYIALDGDLSLSTEDLVNLGKGHYKIKLTSIAEKKVQQSREVIDSIIK
HUTH_HUMAN -----
EPEKYIELDGDRLTTEDLVNLGKGGRYKIKLTPTAEKRVQKSREVIDSIIK
HUTH_CAEEL
ADSLAPMVLAPPTKLLILDGNSLLPEDLVRCEKGECAIQLSMESEDRIKARTFLEKIAS
HUTH_BACS -----
MVTLDGSSLTTADVARVLFDFEEAAASEESMERVKKSRAAVERIVR
HUTH_STRGR -----
MDMHTVVVGTSGTTAEDVVAVARHGARVELSAAAVEALAAARLIVDALAA
HUTH_CORY -----
MASAPQITLGLSGATADDVIAVARHEARISISPOVLEELASVRAHIDALAS

```


Figure 13B

HUTH_PSEPU
EDRTAYGINTGFGLLASTRIASHDLENLQ^RSLVLSHAAGIGAPLDDDLVRLIMVLKINSL
HUTH_RHIME
GNAPVY^GGINTGFGK^LASIKIDSSDVATLQ^RNLILSHCCGVGQPLTEDIVRLIMALKLISL
HUTH_MOUSE
ERTV^VYGITTGFGKFARTVIPANKLQ^ELQVNLV^RSHSSGVGKPLSPERCRMLLALRINVL
HUTH_RAT
ERTV^VYGITTGFGKFARTVIPANKLQ^ELQVNLV^RSHSSGVGKPLSPERCRMLLALRINVL
HUTH_HUMAN
EKT^VVYGITTGFGKFARTVIPINKLQ^ELQVNLV^RSHSSGVGKPLSPERCRMLLALRINVL
HUTH_CAEL
EHRAVYGVTTGFGTFSNVTIPPEK^LKLQ^LNLIRSHATGYGEPLAPNRARMLLALRINIL
HUTH_BACS
DEKTIYGIN^TGFGKFS^DVLIQKEDSAALQ^LNLILSHACGVGDPFPECVSRAMLLLRANAL
HUTH_STRGR
KPEPVYGVSTGFGALASRHIGTELRAQ^LQ^RNIVRSHAAGMGPRVEREVVRALMFLRLKTV
HUTH_CORY
ADTPVYGI^STGFGALATRHIAPE^DRAKLQ^RSLIRSHAAGMGEPVEREVVRALMFLRAKTL

HUTH_PSEPU
SRGFSGIRRKVIDALIALVNAEVYPHIPLKGSV^GASGDLAPLATMSLVLLGEGKARYKGO
HUTH_RHIME
GRGASGVRLELVRLIEAMLDKGVIP^LIPEKGSV^GASGDLAPLAHMAAVMMGHGEAFFAGE
HUTH_MOUSE
AKGY^SGISLET^LKQVIEAFNASCLS^VYVPEKGT^VGASGDLAPLSHLALGLIGEGKMWSPKS
HUTH_RAT
AKGY^SGISLET^LKQVIEVFNASCLS^VYVPEKGT^VGASGDLAPLSHLALGLIGEGKMWSPKS
HUTH_HUMAN
AKGY^SGISLET^LKQVIEMFNASCLP^VYVPEKGT^VGASGDLAPLSHLALGLVGEKMWSPKS
HUTH_CAEL
AKGHS^GISVENIKMIAAFNAFCV^SYVPQ^QGT^VGCSGDLCP^LAHLALGLLGEGKMWSPTT
HUTH_BACS
LKGFS^GVRAELIEQLLAFLNKR^VHPVIP^QQ^QSLGASGDLAPLSHLALALIGQGEVFFEGE
HUTH_STRGR
ASGHTGVRPEVAQTMADV^LNAGITPVVHEYGSLGCSGDLAPLSHCAL^TLMGEGEAEGPDG
HUTH_CORY ASGRS-
VRPVVLET^MVGMLNAGITPVVREY^GSLGCSGDLAPLSHCALVLMGEGEATDAHG

HUTH_PSEPU -
WLSATEALAVAGLEPLTLAAKEGLALLNGTQASTAYALRGLFYAEDLYAAAIACGGLSV
HUTH_RHIME -
RMKGDAAALKAAGLSPVTLAAKEGLALINGTQVSTALALAGL^FRAHRAGQAALITGALST
HUTH_MOUSE
GWADAKYVLEAHGLKPIVLKPK^EGLALINGTQMITSLGCEALERASAIARQADIVAALTL
HUTH_RAT
GWADAKYVLEAHGLKPIVLKPK^EGLALINGTQMITSLGCEAVERASAIARQADIVAALTL
HUTH_HUMAN
GWADAKYVLEAHGLKPVILKPK^EGLALINGTQMITSLGCEAVERASAIARQADIVAALTL
HUTH_CAEL
GWQPADVVLKKNLEPLELGPKEGLALINGTQMV^TALGAYTLERAHNIARQADVIAALS
HUTH_BACS -
RMPAMTGLKKAGIQPVTLTSKEGLALINGTQAMTAMGVVAYIEAEK^LAYQTERIASLTI
HUTH_STRGR
TVRPAGELLAHGIAPVELREKEGLALLNGTDGMLGMLVMALADLRNLYTSADITAALS
HUTH_CORY
DIRPVPELFAEAGLTPVELAEKEGLALVNGTDGMLGQLIMALADLDEL^LDIADATAAMSV

Figure 13C

HUTH_PSEPU EAVLGSRSPPFDARIHE-ARGQRGQIDTAACFRDLLGDSSEVSLSHKNCD-----
KVQDPYS
HUTH_RHIME DAAMGSSAPFHPDIQH-CAAIRARSTRAAALRQLLTG-SPIRQSHIEGDE---
RVQDPYC
HUTH_MOUSE EVLKGTTKAFDTDIHA-VRPHRGQIEVAFRFRSLLDS-
DHPSEIAESHRFCDRVQDAYT
HUTH_RAT EVLKGTTKAFDTDIHA-VRPHRGQIEVAFRFRSLLDS-
DHPSEIAESHRFCDRVQDAYT
HUTH_HUMAN EVLKGTTKAFDTDIHA-LRPHRGQIEVAFRFRSLLDS-
DHPSEIAESHRFCDRVQDAYT
HUTH_CAEL DVLKGTTRAYDPDIHR-IRPHRGONLSALRLRALLHS-
EANPSQIAESHRNCTKVQDAYT
HUTH_BACS EGLQGITDAFDEDIHL-ARGYQEIDVAERIRFYLS-D-SGLTTSQGE-----
LRVQDAYS
HUTH_STRGR EALLGTDKVLAPELHA-IRPHPGQGVSAADNMSRVLAG-SGLTGHHQDDAP---
RVQDAYS
HUTH_CORY EAQLGTDQVFRAELHEPLRPHPGQGRSAQNMFAFLAD-SPIVASHREGDG---
RVQDAYS

HUTH_PSEPU
LRCQPQVMGACLTQLRQAAEVLGIEANAVSDNPLVFAAEGDVISGGNFHAEPVAMAADNL
HUTH_RHIME IRCQPQVDGACLDLLRSVAATLTIEANAVTDNPLVLSDN-
SVVSGGNFHAEPVAFAADQI
HUTH_MOUSE
LRCCPQVHGVVNDTIAFVKDIITTELNSATDNPMVFASRGETISGGNFHGEYPAKALDYL
HUTH_RAT
LRCCPQVHGVVNDTIAFVKDIITTELNSATDNPMVFASRGETISGGNFHGEYPAKALDYL
HUTH_HUMAN
LRCCPQVHGVVNDTIAFVKNIITTELNSATDNPMVFANRGETVSGGNFHGEYPAKALDYL
HUTH_CAEL
LRCVPQVHGVVHDTIEFVREIITTEMNSATDNPLVFADREEIISGGNFHGEYPAKALDFL
HUTH_BACS
LRCIPQVHGATWQTLGYVKEKLEIEMNAATDNPLIFNDGDKVISGGNFHGQPIAFAMDFL
HUTH_STRGR VRCAPQVNGAGRDTLDHAALVAGRELASSVDNPVVLDPG-
RVESNGNFHGAPVAYVLDLFL
HUTH_CORY LRCSPQVTGAARDTIAHARLVATRELAAAIDNPVVLPSG-
EVTSNGNFHGAPVAYVLDLFL

HUTH_PSEPU ALAI AEIGSLSERRISLMMDKHMS-
QLPPFLVENGGVNSGFMIAQVTAALASENKALSH
HUTH_RHIME
ALAVCEIGAISORRIALLVDPALSLRLPAFLAKKPGNSGLMIAEVTSAALMSENKQLSH
HUTH_MOUSE AIGVHELAAISERRIERLCNPSLS-
ELPAFLVAEGGLNSGFMIAHCTAAALVSESKALCH
HUTH_RAT AIGVHELAAISERRIERLCNPSLS-
ELPAFLVAEGGLNSGFMIAHCTAAALVSESKALCH
HUTH_HUMAN AIGIHELAAISERRIERLCNPSLS-
ELPAFLVAEGGLNSGFMIAHCTAAALVSENKALCH
HUTH_CAEL AIAVAELAQMSERRLERLVNKELS-
GLPTFLTPDGGLNSGFMIVQLCAASLVSENKVLCH
HUTH_BACS KIAISELANIAERRIERLVNPQLN-
DLPPFLSHPGLQSGAMIMQYAAASLVSENKTLAH
HUTH_STRGR
AIVAADLGSICERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTQAALVSEMKRLAV
HUTH_CORY
AIAVADLGSIAERRTDRLMLDPARSRDLPAFLADDPGVDSGMMIAQYTQAGLVAENKRLAV

Figure 13D

HUTH_PSEPU	PHSVDSLPTSANQEDHVSMAPAAGKRLWEMAENTRGVPAIEWLGACQGLDLRKG-LKTS
HUTH_RHIME	PASVDSTPTSANQEDHVSMACHGARRLLQMTENLFSIIGIEALAAVQGIEFRAP-LTTS
HUTH_MOUSE	PSSVDSLSTSAATEDHVSMGGWAARKALRVVEHVEQVLAIELLAACQGIEFLRP-LKTT
HUTH_RAT	PSSVDSLSTSAATEDHVSMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRP-LKTT
HUTH_HUMAN	PSSVDSLSTSAATEDHVSMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRP-LKTT
HUTH_CAEEL	PSSVDSIPTSCNQEDHVSMGGFAARKALTVVEHVEAVLAMELLAACQGIEFLKP-LIST
HUTH_BACS	PASVDSIPSSANQEDHVSMGTIAARHAYQVIANTRRVIAIEAICALQAVEYRGI-EHAA
HUTH_STRGR	
PASADSI PSSAMQEDHVSMGWSAARKLRTAVDNLARIVAVELYAATRAIELRAAEGLTPA	
HUTH_CORY	PA-VDSIPSSAMQEDHVSLGWHAARKLPTSVANLRRILAVEMLIAGRALDLRAP-LKPG
HUTH_PSEPU	AKLEKARQALRSEVA-HYDRDRFFAPDIEKAVELLAKG---S-LTGLLPAGVLPSSL---
-	
HUTH_RHIME	PELQKAAAAVRGVSS-SIEEDRYMADDLKAAGDLVASG---R-LAAAVSAGILPKLEN-
HUTH_MOUSE	TPLEKVYDLVRSVVR-
PWIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEKYRMEHIPESR	
HUTH_RAT	TPLEKVYDLVRSVVR-
PWIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEKYRMEHIPESR	
HUTH_HUMAN	TPLEKVYDLVRSVVR-
PWIKDRFMAPDIEAAHRLLEQKVWEVAAPYIEKYRMEHIPESR	
HUTH_CAEEL	APLHKIYQLVRSVAP-
PLNEDRYMKPEIDAVLEMIRENRIWEAVLPHLETLEAMEELDPD	
HUTH_BACS	SYTKQLFQEMRKVVP-SIQQDRVFSYDIERLTDWLKK----ESLIPDHQNKELRGMNI-
HUTH_STRGR	PASEAVVAALRAAGAEGPGPDRFLAPDLAAADTFVREG---R-LVAAVEPVTGPLA---
-	
HUTH_CORY	PATGAVLEVLRSKVA-GPGQDRFLSAELEAAAYDLLANG---S-VHKALEAHLPE-----
-	
HUTH_PSEPU	-----
HUTH_RHIME	-----
HUTH_MOUSE	PLSPTAFSLESLRKNSATIPESDDL----
HUTH_RAT	PLSPTAFSLESLRKNSATIPESDDL----
HUTH_HUMAN	PLSPTAFSLQFLHKKSTKIPESEDL----
HUTH_CAEEL	ALRQFTKTPTGIVQDRSMIPISDDEESIE
HUTH_BACS	-----
HUTH_STRGR	-----
HUTH_CORY	-----

Figure 14A

1	100.0%	80
983831		
1 SWALL: CAC21618	66.1%	MASAPQITLGLSGATADDVIAVARHEARISISPOVLEELASVRAHIDALASADTPVYIGISTGFGALATRHIAPEDRAKLQ
2 SWALL: HUTH_STRGR	65.4%	---MHTVVVGTSGVTASDVLAVARAGARIELSEEAVALAAARSVVDALAAKPDPPVYGVSTGFGALATRHISPELRGRLQ
3 SWALL: HUTH_DEIRA	46.8%	-MDMHTVVVGTSGTAEEDVAVARHGARVELSAAAVEALAAARLIVDALAAKPEPVYGVSTGFGALASRHIGTELRAQLQ
4 SWALL: BAB16159	42.0%	-----MILDRDLNLEQFISVVRHGEQVELSAAARERARARTVIEQIVEGDTPIYGVNTGFGKFEFENVQIDRSQLAQLQ
5 SWALL: Q9KWE4	42.0%	-----VPLHHLADIYNNNGSAKLDPSFDAAVLKGAAARIAEIAAGNAPVYGINTEGFGKLASIKIDAADLALTLQ
6 SWALL: HUTH_BACSU	40.4%	-----VPLHHLADIYNNNGSAKLDPSFDAAVLKGAAARIAEIAAGNAPVYGINTEGFGKLASIKIDAADLALTLQ
7 SWALL: Q9KSQ4	42.2%	----MVTLDGSSLTADVARVLFEEAAAEESEMERVKKSRAAVERIVRDEKTIYGINTEGFGKFSVDVLIQKEDSAAALQ
8 SWALL: Q9HU85	41.7%	---MLHLMIKPGQLSLKQLRQVRSFVLSLDPEAI PAIAESAQVVEQVISEGRTVYGINTEGFGLLANTKIAPODLETLQ
9 SWALL: Q9KBE6	39.3%	----MTNLKLLDGRSLSLHDLHRIIYEGETVGADESMEKVKQSRKAVEQIVADEKIIYGITTEGFGKFSDFIDPDDVENVLQ
10 SWALL: HUTH_PSEPU	41.7%	----TELTLPKPGTLT LAQLRAIHAAPVRLQDASAPPAIDASVACVEQIIAEDRTAYGINTEGFGLLASTRIASHDLENLQ
11 SWALL: HUTH_RHIME	40.6%	-----LRPGSVPLSDLETIYWTGAPARLDAEDAGIAKAAARIAEIVAGNAPVYGINTEGFGKLASIKIDSSDVATLQ
12 SWALL: Q9HU90	40.7%	MSDLPVVVFGDGLRWQELVAVARHGARLELSAAAWARIDNARAIVCRIVANGERAYGISTGLGALCDVLLLEGEQLAELS
13 SWALL: HUTH_HUMAN	39.2%	KYREPEKYIELDGLTTEDLVNLGKGRYKIKLTPTAEKRVQKSREVIDSIIKEKTVVYGITTEGFGKFA-RTVPIPNKLLQLQ
14 SWALL: HUTH_CAEEL	38.8%	VLAPPTKLLILDGNSPEDLVRCEKGECAIQLSMESEDRIRKARTFLEKIASSEHRAVYGVTTGFGTFSNVTIIPPEKLLKKLQ
15 SWALL: Q9HLI6	41.0%	----MIEIDGRSLRVEDVYAVAVEYDRVSI SDDTLKAVEEKHEAFLKLNKINSKTVYGVNTGFGSLLNVHIERDQEIQLQ
16 SWALL: HUTH_MOUSE	38.6%	KYREPEKYIALDGDSTEDLVNLGKGRYKIKLTSIAEKKVQOSREVIDSIIKERTVVYGITTEGFGKFA-RTVPIPNKLLQLQ
17 SWALL: BAB29407	38.6%	KYREPEKYIALDGDSTEDLVNLGKGRYKIKLTSIAEKKVQOSREVIDSIIKERTVVYGITTEGFGKFA-RTVPIPNKLLQLQ
18 SWALL: HUTH_RAT	38.2%	KYREPEKYIALDGDSTEDLVNLGKGRYKIKLTSIAEKKVQOSREVIDSIIKERTVVYGITTEGFGKFA-RTVPIPNKLLQLQ
19 SWALL: AAG53586	39.8%	---MNALTLTPGTLT LAQLRQVWQPLQLTLDESHEAINDSVACVEAIVAEGRRTAYGINTEGFGLLAQTRIAATHDLENLQ
20 SWALL: Q9KKE0	38.9%	----MGEMISLDGPLTWREIASIAEGASLDLSPARLRIAQARRIVDALVERGIRGYGINTEGFGALCDVVISRENQQALS
21 SWALL: Q9HQD5	42.2%	-----MSDTRIDAADREALQ

Figure 14B

983831	100.0%	1	RSLIRSHAAGMGEPPERVVRALMFLRAKTIASGRRTGVRPVVLETMVGMNAGITPVVREYGSGLGCSGDLAPLSHCALVL	160
1 SWALL: CAC21618	66.1%		RNIVRSHAAGMGPVEREVVRALMFLRLKTVCSGRRTGVRPEVAQTMADVINAQITPVVHEYGSGLGCSGDLAPLSHCALTL	
2 SWALL: HUTH_STRGR	65.4%		RNIVRSHAAGMGPVEREVVRALMFLRLKTVASGHTGVRPEVAQTMADVINAQITPVVHEYGSGLGCSGDLAPLSHCALTL	
3 SWALL: HUTH_DEIRA	46.8%		HNLIVSHAIGMGEPLPAEVRVGMLLRAQSLSLGHSGVRVEVELLALLNADALPVVPSQGSVGSAGDPLAPLAHLALGL	
4 SWALL: BABI16159	42.0%		RNLI LSHCCGVGAPLPENVVRLLMALKLISLGRGASGVRLELRLIEGMLEKGVIPVPEKGSVGSAGDPLAPLAHMSATM	
5 SWALL: Q9KWE4	42.0%		RNLI LSHCCGVGAPLPENVVRLLMALKLISLGRGASGVRLELRLIEGMLEKGVIPVPEKGSVGSAGDPLAPLAHMSATM	
6 SWALL: HUTH_BACSU	40.4%		RNLI LSHACGVGDFPECVSRAMLLLRANALLKGFSGVRAELIEQLLAFLNKRVRHPVIPPQQGSLGASGDLAPLSHLALAL	
7 SWALL: Q9KSQ4	42.2%		KSIVLSHAAGIGELMSDETIVRLMMLLKINSLARGYSGIRLEVIQALIELVNNQIYPCVPKKGSVGSAGDPLAPLAHMSATM	
8 SWALL: Q9HU85	41.7%		RSIVLSHAAGVGEALDDAMVRLVMLLKVNLSLARGFSGIRRKVIDALIALINAEVYPHIPLKGSVGSAGDPLAPLAHMSLVL	
9 SWALL: Q9KBE6	39.3%		HNLIVSHAAGVGSPPFETVSRMTLVLRANALLKGFSGVRPLVIERLLALVNAIHPVIPPQQGSLGASGDLAPLSHLALVL	
10 SWALL: HUTH_PSEPU	41.7%		RSLVLSHAAGIGAPLDDDLVRLIMVLKINLSRGSFSGIRRKVIDALIALVNAEVYPHIPLKGSVGSAGDPLAPLAHMSLVL	
11 SWALL: HUTH_RHIME	40.6%		RNLI LSHCCGVGQPLTEDIVRLIMALKLISLGRGASGVRLELVRLIEAMLDKGVIPVPEKGSVGSAGDPLAPLAHMAAVM	
12 SWALL: Q9HU90	40.7%		RNTLLSHACGVGEPLRDEQTRAIICAAVANYSQKSGDRSLVEGLLALLNHGITPQVPAQGSVGY --LTHMAHVGIAL	
13 SWALL: HUTH_HUMAN	39.2%		VNLVRSHSSGVGKPLSPERCMLLALRINVLAKGYSGISLETLKQVIEAFNASCLPYVPEKGTVGASGDLAPLSHLALGL	
14 SWALL: HUTH_CAEEL	38.8%		LNLI RSHATGYGEPLAPNRARMLLALRINILAKGHSGISVENIKKMI AAFNAFCVSYVPPQGTVCSCGDLAPLSHLALGL	
15 SWALL: Q9HLI6	41.0%		KNLIRSHSSGVGDYLENRYVRALMVRNLNLAAGYSAVSADLLNMMVEMLNDRDVI PAVPKYGSVGSAGDPLAPLAHIGLAM	
16 SWALL: HUTH_MOUSE	38.6%		VNLVRSHSSGVGKPLSPERCMLLALRINVLAKGYSGISLETLKQVIEAFNASCLSYVPEKGTVGASGDLAPLSHLALGL	
17 SWALL: BAB29407	38.6%		VNLVRSHSSGVGKPLSPERCMLLALRINVLAKGYSGISLETLKQVIEAFNASCLSYVPEKGTVGASGDLAPLSHLALGL	
18 SWALL: HUTH_RAT	38.2%		VNLVRSHSSGVGKPLSPERCMLLALRINVLAKGYSGISLETLKQVIEAFNASCLSYVPEKGTVGASGDLAPLSHLALGL	
19 SWALL: AAG53586	39.8%		RSLVLSHAAGVGEPLDDDIVRLMMVLKINSLARGFSGIRLSVIQALIALVNAEVYSDPAKGSVGSAGDPLAPLAHMSLTL	
20 SWALL: Q9KKE0	38.9%		RNIILSHACGVGDPPLGRVEARAVMAAQIANLTHGYSVVRVETAEMLLALLNADIIPVPSRGSVGY ----LTHAALVL	
21 SWALL: Q9HQD5	42.2%		ANLVRSHAAGAGSELDTAAVRALLVTRLNALAKGYSGIRERERVDVIVGLLNEGVRHPVVPVPSRGRSLGASGDLAPLAHMSRVL	

Figure 14C

	161	2	240
983831	100.0%		
1 SWALL: CAC21618	66.1%		
2 SWALL: HUTH_STRGR	65.4%		
3 SWALL: HUTH_DEIRA	46.8%		
4 SWALL: BAB16159	42.0%		
5 SWALL: Q9KWE4	42.0%		
6 SWALL: HUTH_BACSU	40.4%		
7 SWALL: Q9KSQ4	42.2%		
8 SWALL: Q9HU85	41.7%		
9 SWALL: Q9KBE6	39.3%		
10 SWALL: HUTH_RHIME	41.7%		
11 SWALL: HUTH_RHIME	40.6%		
12 SWALL: Q9HU90	40.7%		
13 SWALL: HUTH_HUMAN	39.2%		
14 SWALL: HUTH_CAEEL	38.8%		
15 SWALL: Q9HLI6	41.0%		
16 SWALL: HUTH_MOUSE	38.6%		
17 SWALL: BAB29407	38.6%		
18 SWALL: HUTH_RAT	38.2%		
19 SWALL: AAG53586	39.8%		
20 SWALL: Q9KKE0	38.9%		
21 SWALL: Q9HQD5	42.2%		

[MGEGEATDAHGDIRVPPELFAEAGLTPVELAEKEGLALVNGTDCMLGQIMALADLDELDDIADATAAMSVEAQLGTDQV
MGEEDAEGPDGTVRPA GELLAAHGIAPVELREKEGLALLNGTDCMLGMLVMALADLDTLYKSADITAAALTMEALLGTDREV
MGEGEAEGPDGTVRPA GELLAAHGIAPVELREKEGLALLNGTDCMLGMLVMALADLRLNLYTSADITAAALSLEALLGTDKV
IGLGDI-EYQGVQVRPAADVLAELGLSPVQLQAKEGLALINGTQLMGSLALALHDAQVLLGTANLAAAMTVEARYGSHRP
MGEGEAF-YQGVQMPKDALAKAGLSPVVLAAKEGLALINGTQSTALALAGLFRHRAAQSALVTGALSTDAAMGSSAP
MGEGEAF-YQGVQMPKDALAKAGLSPVVLAAKEGLALINGTQSTALALAGLFRHRAAQSALVTGALSTDAAMGSSAP
IGQGEVF-FEGERPAMTGLKKAGIQPVTLT SK EGLALINGTQAMTAMGVVWAYIEAEKLAYQTERIASLTIEGLQGIIDA
LGEQAR-YNGKIISGLEAMKIAGLEPITLAPKEGLALINGTQASTAFALGLFVAEDLFA SATVCGAMSVEAALGSRRP
IGESRARH-RGEWLPAAEALAVAGLEP LTLAAKEGLALINGTQVSTAYALRGLFEAEDLFAAATVCGGLSVEAMLGSRAP
LGEGEVF-YKGTKTASFALKEEIEPIFLTAKEGLALINGTQAMTAMGVVWAYIEAEKLAFAQSEIIASLTMEGLRGIIDA
LGEGKAR-YKGQWLSATEALAVAGLEP LTLAAKEGLALINGTQASTAYALRGLFYAEDLYAAAACGGLSVEAVLGSRSP
MGHGEAFFAGERMKGDAALKA-AGLSPVTIAAKEGLALINGTQVSTALALAGLFRHRAAQSALVTGALSTDAAMGSSAP
LGIGEVSYRGSVVPAAAALAAEGLATVRLGAKDGLCLVNGT PCMTGLACLALDDAQR LAQWADVIGAMSF EALRGQLAA
VGEKMWSPKSGWADAKYVLEAHGLKPVILKPK EGLALINGTQMITSLGCEAVERASAIARQADIVAALTLLEV LKGTTKA
LGEKMWSPPTGWQPADVVLKKNLEP LELGPK EGLALINGTQMV TALGAYTLERAHNIARQADVIAALS LDV LKGTTRA
MGEKAF-FEGR LMSARALEKAGLKP YQFKEKEGVALINGT SFMSGILSIAVMDAHDILENAIR SALLSFEALGGT SKA
IGEGKMWSPKSGWADAKYVLEAHGLKPIVLKPK EGLALINGTQMITSLGCEALERSAIARQADIVAALTLLEV LKGTTKA
IGEGKMWSPKSGWADAKYVLEAHGLKPIVLKPK EGLALINGTQMITSLGCEALERSAIARQADIVAALTLLEV LKGTTKA
IGEGKMWSPKSGWADAKYVLEAHGLKPIVLKPK EGLALINGTQMITSLGCEAVERASAIARQADIVAALTLLEV LKGTTKA
LGEGKAR-YRGEWLPAAALQKAGLAPVTLAAKEGLALINGTQASTAFALRGLFEAEDLFA SAVVCGAL TTEAVLGSRRP
IGHGSAMQGTERLSGADAL-ARLGLAPLRLEAKEGLSLVNGT PCATGLAALALARTERLFAWADAAAAMTYE-NLGSQAN
IGEGQA-DVAGERMPAAEALAAADLEPVTIQAKEGLALINGTQLTGVAALALVDAERVLR SADTAGAL TTEVTMSTTAS

Figure 14D

983831		241	:	3	.	320
1	SWALL: CAC21618	100.0%	[FRAELHEPLRPHPGQGRSAQNMEFLADSPIVASHREGDGRVQDAYSLRCSQPVTGAARDTIAHARLLVATRELAATAIDNP	.	
2	SWALL: HUTH_STRGR	66.1%		LAPELHA-IRPHPGQAASAANMAAVLKGSLTGHQDDAPRVQDAYSVRCAPQVAGAGRDTMAHAGLVAERELAAAVDNP	.	
3	SWALL: HUTH_DEIRA	65.4%		LAPELHA-IRPHPGQVSADNMSRVLGSLTGHQDDAPRVQDAYSVRCAPQVNGAGRDTLDHAALVAGRELASSVDNP	.	
4	SWALL: BAB16159	46.8%		FQPDV-VGLRPHGALAVAAELREFLAGSEIAPSHLTGDKVQDAYSLRAVPQVHGATWDALAQAEERVLAVEFASVTDNP	.	
5	SWALL: Q9KWE4	42.0%		FHPDIHT-LRGHKGQIDAGSALRNLLQSGEIRESHIEGDERVQDPCIRCPQVQDQACLDLLASVARTLEIEANAVTDNP	.	
6	SWALL: HUTH_BACSU	42.0%		FHPDIHT-LRGHKGQIDAGSALRNLLQSGEIRESHIEGDERVQDPCIRCPQVQDQACLDLLASVARTLEIEANAVTDNP	.	
7	SWALL: Q9KSQ4	40.4%		FDEDIHLA-RGYQEIQIDVAERIRFYLSDSGLTTS--QGELRVQDAYSLRCPQVHGATWTLGYVKEKLEIEMNAATDNP	.	
8	SWALL: Q9HU85	42.2%		FDPRIHR-VRGHRQMDAATAYRHLVSSSEIGQSHSNCE-KVQDPYSLRCPQVQMGACLDLQIRSAEVEVEANSVSDNP	.	
9	SWALL: Q9KBE6	41.7%		FDARIHAA-RQQRGQIDVAAAYRDLLASSEVARSHKCD-KVQDPYSLRCPQVQMGACLDLQIRSAEVEVEANSVSDNP	.	
10	SWALL: HUTH_PSEPU	39.3%		FDEQIHFA-RGYVEQVDVARRMESYLQDSQLTT--RQGELRVQDAYSLRCPQVHGATWTLRYVKEKLEIEMNAATDNP	.	
11	SWALL: HUTH_RHIME	41.7%		FDARIHEA-RGQRGQIDTAACFRDILLGDSSEVSSHKNCD-KVQDPYSLRCPQVQMGACLDLQIRSAEVEVEANSVSDNP	.	
12	SWALL: Q9HU90	40.6%		FHPDIHQCAAIRARSTRAAA-LRQLLTGSPIRQSHIEGDERVQDPCIRCPQVQDQACLDLLRSVAATLTIEANAVTDNP	.	
13	SWALL: Q9HU90	40.7%		FDAEI-VALKPHGMQRVAANLRALLAGSQVLENAR--GIRTQDALSIRSIPQIHGACRDLAHARQIET-ELNSATDNP	.	
14	SWALL: HUTH_HUMAN	39.2%		FDTDIHA-LRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHGAVVNDTIAFVKDIIITTELSATDNP	.	
15	SWALL: HUTH_CAEEL	38.8%		YDPDIHR-IRPHRGQNLALRLRALLNPSQIAESHRNCT-KVQDAYTLRCPQVQVHGVDHTIEFVREIITTEMSATDNP	.	
16	SWALL: Q9HLI6	41.0%		FTPWILGA-RPHLGQVAIGNRFRREYLTGSDIV--KRADSVKQVQDAYTLRCPQVYGSVADVIDYVENVLSVEINSATDNP	.	
17	SWALL: HUTH_MOUSE	38.6%		FDTDIHA-VRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHGAVVNDTIAFVKDIIITTELSATDNP	.	
18	SWALL: BAB29407	38.6%		FDTDIHA-VRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHGAVVNDTIAFVKDIIITTELSATDNP	.	
19	SWALL: HUTH_RAT	38.2%		FDTDIHA-VRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHGAVVNDTIAFVKDIIITTELSATDNP	.	
20	SWALL: AAG53586	39.8%		FDARIHE-VRGQRGQIDAAALFRHVLTDTSALASHHNCNCD-KVQDPYSLRCPQVQMGACLDLQIRSAEVEVEANSVSDNP	.	
21	SWALL: Q9KKE0	38.9%		AFaelPLALRQSPGLSAVGEGLRDWLADSPMLAG--TAGTRTQDPLSLRAVPQVHGAAARDAFGQVAEIVDRELASVTDNP	.	
22	SWALL: Q9HQD5	42.2%		CAPAIHE-VRPHDGGQAVSARHIRNLTAGSEVLDHHRDCCD-RVQDAYSIIRCLPQVHGAVRDALDHLRAAVATELSATDNP	.	

Figure 14E

		321	:	400
983831		100.0%		VVLPSEVTSNGNFHGPVAVYVLDLAVAVADLGSIAERRTDRMLDPARSRDLPAFLADDPGVDSGMMIAQYTOAGLVAE
1	SWALL: CAC21618	66.1%		VVLPDGRVESNGNFHGPVAVYVLDLAVAVADLGSIAERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTOAALVGE
2	SWALL: HUTH_STRGR	65.4%		VVLPDGRVESNGNFHGPVAVYVLDLAVAVADLGSICERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTOAALVSE
3	SWALL: HUTH_DEIRA	46.8%		LIFPTGEVVSNGNFHGPVAVYVLDLAVAVADLGSISERRTEQLLNPAALS-GLPAFLTPNGGLNSGFMIAQYTSAAALVSE
4	SWALL: BAB16159	42.0%		LVLSDNSVVSNGNFHGPVAVYVLDLAVAVADLGSIAERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTSAAALVSE
5	SWALL: Q9KWE4	42.0%		LVLSDNSVVSNGNFHGPVAVYVLDLAVAVADLGSIAERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTSAAALVSE
6	SWALL: HUTH_BACSU	40.4%		LIFNDGDVVSNGNFHGPVAVYVLDLAVAVADLGSIAERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTSAAALVSE
7	SWALL: Q9KSQ4	42.2%		LVFADGDIISNGNFHGPVAVYVLDLAVAVADLGSIAERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTSAAALVSE
8	SWALL: Q9HU85	41.7%		LVFAAGDVISSNGNFHGPVAVYVLDLAVAVADLGSIAERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTSAAALVSE
9	SWALL: Q9KBE6	39.3%		LIFDNGQVVSNGNFHGPVAVYVLDLAVAVADLGSIAERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTSAAALVSE
10	SWALL: HUTH_PSEPU	41.7%		LVFAAGDVISSNGNFHGPVAVYVLDLAVAVADLGSIAERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTSAAALVSE
11	SWALL: HUTH_RHIME	40.6%		LVLSDNSVVSNGNFHGPVAVYVLDLAVAVADLGSIAERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTSAAALVSE
12	SWALL: Q9HU90	40.7%		LLLGTPEVVSQANPHGESVAVAMAADLLAVAVADLGSIAERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTSAAALVSE
13	SWALL: HUTH_HUMAN	39.2%		MVFANGETVSSNGNFHGPVAVYVLDLAVAVADLGSIAERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTSAAALVSE
14	SWALL: HUTH_CAEEL	38.8%		LVFADREIISNGNFHGPVAVYVLDLAVAVADLGSIAERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTSAAALVSE
15	SWALL: Q9HLI6	41.0%		L-FNGEEVVSNGNFHGPVAVYVLDLAVAVADLGSIAERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTSAAALVSE
16	SWALL: HUTH_MOUSE	38.6%		MVFAASGETISSNGNFHGPVAVYVLDLAVAVADLGSIAERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTSAAALVSE
17	SWALL: BAB29407	38.6%		MVFAASGETISSNGNFHGPVAVYVLDLAVAVADLGSIAERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTSAAALVSE
18	SWALL: HUTH_RAT	38.2%		MVFAANEMVFRNGNFHGPVAVYVLDLAVAVADLGSIAERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTSAAALVSE
19	SWALL: AAG53586	39.8%		AVAGSPEVHSQAHAHVAALGLAMDSLAVAVAEVAAISERRIDRLVNPLVS-GLPAFLVAGDSVSSGFMIAQYTTAAALVSE
20	SWALL: Q9KKE0	38.9%		LVFPGTIVVSNGNFHGPVAVYVLDLAVAVADLGSIAERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTTAAALVSE
21	SWALL: Q9HQD5	42.2%		LVFPGTIVVSNGNFHGPVAVYVLDLAVAVADLGSIAERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTTAAALVSE

Figure 14F

	983831	401	480
1	SWALL:CAC21618	100.0%	NKRLAVPASVDSIPSSAMQEDHVSGLGWHAAARKLRTSVANLRRILAVEMLIAGRALDLRAPLKPGPATGAVLEVLRSKVAG
2	SWALL:HUTH_STRGR	66.1%	LKRLAVPASADSI PSSAMQEDHVS MGWSAARKLRTAVDNLARVIAVELYAAATRAIQRLREGLTPAPASQAVVEAVRAAVEG
3	SWALL:HUTH_DEIRA	65.4%	MKRLAVPASADSI PSSAMQEDHVS MGWSAARKLRTAVDNLARIVAVELYAAATRAIELRAALTPAPASEAVVAALRAAGAG
4	SWALL:BAB16159	46.8%	NKVL SHPASVDSIPT SANQEDHVS MGHAARQLRQIVANVQTVLSIELLCAAQGLDFQQ-LRAGRGVQAAAYEYVRTFVPT
5	SWALL:Q9KWE4	42.0%	NKQMSHPASVDSIPT SANQEDHVS MACHGARRLLAMTDNLFGLGIEALAAVQGVLELRGPKLTSPELEKAAAVALRSAPV
6	SWALL:HUTH_BACSU	42.0%	NKQMSHPASVDSIPT SANQEDHVS MACHGARRLLAMTDNLFGLGIEALAAVQGVLELRGPKLTSPELEKAAAVALRSAPV
7	SWALL:Q9KSQ4	40.4%	NKTLAHPASVDSIPT SANQEDHVS MGTIARHAYQVIANTRRVIAIEAICALQAVEYRGIEHAASYTKOLFQEMRKVVPS
8	SWALL:Q9HU85	42.2%	NKTLAHPASVDSIPT SANQEDHVS MATFAARRLRDMGENTRGI LAVEYLAAAQGLDFRAPLKSPPRIIEEARQILREKVPF
9	SWALL:Q9KBE6	41.7%	NKALAHPASVDSIPT SANQEDHVS MAPNAGKRLWAMAENVRGILAVEWLGACQGLDFERGLKSSPKLEQARRLLRDKVPY
10	SWALL:HUTH_PSEPU	39.3%	NKTLAHPASVDSIPT SANQEDHVS MGTIGSRHAYQI IQNVRNVLAIEILICAMQAVDIRGREKMASFTKKILEKGREHVPY
11	SWALL:HUTH_RHIME	41.7%	NKALSHPHSVDSIPT SANQEDHVS MAPAAGKRLWEMAENTRGLVAIEWLGACQGLDLRKLKTSAKLEKARQALRSEVAH
12	SWALL:Q9HU90	40.6%	NKQLSHPASVDSIPT SANQEDHVS MACHGARRLLQMTENLFSIIGIEALAAVQGVLEFRAPLTSPELQKAAAARVGVSSS
13	SWALL:HUTH_HUMAN	40.7%	NRQLAQPAVVDNFVTSALQEDHLSLGTSAALKLGRALENLRRILAEIYLLAAQAFEFLLAPQRFQGTAAAWGILRERVPA
14	SWALL:HUTH_CAEEL	39.2%	NKALCHPSSVDSIPT SAATEDHVS MGGWAARKALRVIEHVEQVLAIELLAACQGVLEFRPLKTTTTPLEKVVYDLVRSVVRP
15	SWALL:Q9HLI6	38.8%	NKVLCHPSSVDSIPT SCNQEDHVS MGGFAARKALTVVEHVEAVLAMELLAACQGVLEFLKPLIISTAPLHKIYQLVRS-VAP
16	SWALL:HUTH_MOUSE	41.0%	NKVLAYPSSADTIPT SANQEDHVS MGTGSLKLEI IDNVRYIIAIEYLLGSQALEFTDK-GMSPSTRKIYKIREKVEK
17	SWALL:BAB29407	38.6%	SKALCHPSSVDSIPT SAATEDHVS MGGWAARKALRVVEHVEQVLAIELLAACQGVLEFRPLKTTTTPLEKVVYDLVRSVVRP
18	SWALL:HUTH_RAT	38.6%	SKALCHPSSVDSIPT SAATEDHVS MGGWAARKALRVVEHVEQVLAIELLAACQGVLEFRPLKTTTTPLEKVVYDLVRSVVRP
19	SWALL:AAG53586	38.2%	SKALCHPSSVDSIPT SAATEDHVS MGGWAARKALRVIEHVEQVLAIELLAACQGVLEFRPLKTTTTPLEKVVYDLVRSVVRP
20	SWALL:Q9KKE0	39.8%	NKGLCHPPTSVDK-PPSANQEDHVS MAPAAGRRLWEMAGNTRGVLAWEWLAACQGVADLRDGLTSSPLLEQARQSCGEQVAH
21	SWALL:Q9HQD5	38.9%	NRRLLAAPASLDGGITSAIQEDMLTHATPAAWKALSIVDNLERILAEIELLAHHRPMSCSRKRARRRNAPLPTTGTYYARRSP
		42.2%	LRSLGQP-TLDNASVSGAQEDHVS MSAGAAYNFREAVEKAATVVGVVELLCCGAQGREFLDPLALGAGTAAAYDLVR-EVSE

Figure 14G

983831		481		[.	5	.]	513
1	SWALL:CAC21618	100.0%		PGQDRFLSAELEAAAYDLLANGSVHKALEAHLPA					
2	SWALL:HUTH_STRGR	66.1%		PGPDRHLAPDLAAADAFVRAGHLVAAAESVTGP					
3	SWALL:HUTH_DEIRA	65.4%		PGPDRFLAPDLAAADTFVREGRLVAAVEPVTGP					
4	SWALL:BAB16159	46.8%		LTEDRYFRPDLRLRGELVSGRVAQAADTQAPA					
5	SWALL:Q9KWE4	42.0%		LEDDRYMATDLKAAIEVVASGALVSAISSGLPV					
6	SWALL:HUTH_BACSU	42.0%		LEDDRYMATDLKAAIEVVASGALVSAISSGLPV					
7	SWALL:Q9KSQ4	40.4%		IQQDRVFSYDIERLTDWLKESLI PDHQNKELR					
8	SWALL:Q9HU85	42.2%		YKDRYFAPDIEKANALL-QLAVHNRLMPDQLL					
9	SWALL:Q9KBE6	41.7%		YQEDRFFAPDIEAASQLLASGCLNALLPARLLP					
10	SWALL:HUTH_PSEPU	39.3%		IDQDRMFAKDIERAAKWLKDGSDFTKMREKER					
11	SWALL:HUTH_RHIME	41.7%		YDRDRFFAPDIEKAVELLAKGSLTGLLPAGLPS					
12	SWALL:Q9HU90	40.6%		IEEDRYMADDLKAAGDLVASGRLAAAVSAGLPK					
13	SWALL:HUTH_HUMAN	40.7%		YDTRWLAPDIASAAAILGERKSLARLAASIGD					
14	SWALL:HUTH_CAEEL	39.2%		WIKDRFMAPDIEAAHRLLEQKVWEVAAPYIEK					
15	SWALL:Q9HLI6	38.8%		PNEDRYMKPEIDAVLEMIRENRIWEAVLPHLET					
16	SWALL:HUTH_MOUSE	41.0%		LDHDRPPSFDIETIRKMMDKKEFISALP-----					
17	SWALL:BAB29407	38.6%		WIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEK					
18	SWALL:HUTH_RAT	38.6%		WIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEK					
19	SWALL:AAG53586	38.2%		WIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEK					
20	SWALL:Q9KKE0	39.8%		YDDDRFFAPDIEAAISLLNKGSLVGLLP AFL--					
21	SWALL:Q9HQD5	38.9%		PIATIVR-----					
		42.2%		PAGDRALADDMAAVGDLVLRAGLVEDAVARALDA					

Figure 14H**KEY:**

983831 : HAL
1 CAC21618 : Streptomyces coelicolor
2 HUTH_STRGR : Streptomyces griseus
3 HUTH_DEIRA : Deinococcus radiodurans
4 BAB16159 : Agrobacterium rhizogenes
5 Q9KWE4 : Agrobacterium rhizogenes
6 HUTH_BACSU : Bacillus subtilis
7 Q9KSQ4 : Vibrio cholerae
8 Q9HU85 : Pseudomonas aeruginosa
9 Q9KBE6 : Bacillus halodurans
10 HUTH_PSEPU : Pseudomonas putida
11 HUTH_RHIME : Rhizobium meliloti
12 Q9HU90 : Pseudomonas aeruginosa
13 HUTH_HUMAN : Human
14 HUTH_CAEEL : Caenorhabditis elegans
15 Q9HLI6 : Thermoplasma acidophilum
16 HUTH_MOUSE : Mouse
17 BAB29407 : Mus musculus (Mouse)
18 HUTH_RAT : Rat
18 AAG53586 : uncultured bacterium pCosAS1
20 Q9KKE0 : Rhizobium meliloti
21 Q9HQD5 : Halobacterium sp

Figure 15A

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STRG 6 VVVGTSGTTAEDVVAVARHGARVELSAAAVEALAAARLIVDALAAKPEPVYGVSTGFGAL
"HAL" 7 ITLGLSGATADDVIAVARHEARISISPQVLEELASVRAHIDALASADTPVYGI STGFGAL
      * ** ** ** ** ** ** ** ** ** ** ** ** ** **   * ** **   * ** **   * ** **   * ** **   *
STRG, 66 ASRHIGTELRAQLQRNIVRSHAAGMGRVEREVVRALMFLRLKTVASGHTGVRPEVAQTM
HAL    67 ATRHIAPEDRAKLRSLIRSHAAGMGEPEVEREVVRALMFLRAKTLASGRTGVRPVVLETM
      * ** ** * ** ** * ** ** * ** ** * ** ** * ** ** * ** ** * ** ** * **
STRG 126 ADVLNAGITPVVHEYGSLGCSGDLAPLSHCAL TLMGEGEAE GPDGTVRPAGELLAAHGIA
HAL    127 VGMLNAGITPVVREYCSL GCSGDLAPLSHCALVLMGEGEATDAHGDIRPVPELFAEAGLT
      * ** ** * ** ** * ** ** * ** ** * ** ** * ** ** * ** ** * ** ** *
STRG 186 PVELREKEGLALLNGTDGMLGMLMALADLRNLYTSADITAAALSLEALLGTDKVLAPELH
HAL    187 PVELAEKEGLALVNGTDGMLGQLIMALADLDELDDIADATAAMSVEAQLGTDQVFRAELH
      * ** ** * ** ** * ** ** * ** ** * ** ** * ** ** * ** ** * ** ** *
STRG 246 A-IRPHPGQVSADNMSRVLAGSGLTGHHQDDAPRVQDAYSVRCAPQVNGAGRDTLDHAA
HAL    247 EPLRPHPGQGRSAQNMFAFLADSPIVASHREGDGRVQDAYSLRCSPOVTGAARDTIAHAR
      * ** ** * ** ** * ** ** * ** ** * ** ** * ** ** * ** ** * ** ** *
STRG 305 LVAGRELASSVDNPPVLPDGRVESNGNFHGAPVAYVLDFLAIVAADLGSICERRTRDLLD
HAL    307 LVATRELAAAI DNPVLPVPSGEVTSNGNFHGAPVAYVLDFLAIAVADLGSIAERRTRMLD
      * ** ** * ** ** * ** ** * ** ** * ** ** * ** ** * ** ** * ** ** *

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Figure 15B

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STRG 365 KNRSGLPPFLADDAGVDSGLMIAQYTQAALVSEMKR LAVPASADSI PSSAMQEDHVS MG
HAL 367 PARSRDLPAFLADDPGVDSGMMIAQYTQAGLVAENKR LAVPASVDSI PSSAMQEDHVS LG
** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** *
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STRG 425 WSAARKLRTAVDNLARI VAVELYAATRAIELRAEGLTPAPASEAVVAALRAAGAE GPGP
HAL 427 WHAARKLRTSVANLRRILAVEMLIAGRALDLRAP--LKP GPATGAVLEVLRSKVA-GPG Q
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
STRG 485 DRFLAPDLAAADTFVREGRLVAAVE
HAL 484 DRFLSAELEAAAYDLLANGSVHKALE
* * * * * * * * * * * * *

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CLONING, OVEREXPRESSION AND THERAPEUTIC USE OF BIOACTIVE HISTIDINE AMMONIA LYASE

This Application claims the benefit of provisional appli- 5
cation 60/197,770, filed Apr. 14, 2000 now abandoned.

FIELD OF THE INVENTION

The present invention relates generally to bioactive, 10
amino acid-degrading enzymes, more specifically to a his-
tidine ammonia lyase derived from a bacterium belonging to
the family Corynebacteriaceae, and to conservative variants
thereto. Also described is the use of histidine ammonia
lyase, singly or combined with L-histidinol, for treating
various viral diseases. 15

BACKGROUND OF THE INVENTION

Histidine ammonia lyase (EC 4.3.1.3) catalyzes the con-
version of L-histidine to urocanic acid and ammonia. This is
the first step in the degradation of histidine in both mammals
and bacteria. A deficiency in this enzyme results in
histidinemia, which is characterized by high serum histidine
levels.

An isolated histidine ammonia lyase enzyme is one agent 25
for treating increased histidine levels. Several lines of evi-
dence indicate that in vivo depletion of serum histidine
concentrations by histidine ammonia lyase could have addi-
tional therapeutic value. For example, histidine ammonia
lyases have been shown in in vivo animal models to have
potential therapeutic value against certain tumors. Roberts et
al., *Cancer Treat. Rep.* 63:1045 (1979); Jack et al., *Leukemia*
Res. 7:421 (1983).

Therapeutically useful (bioactive) enzymes generally dis- 35
play characteristics that are predictors of usefulness in vivo.
These factors are outlined in Holcenberg and Roberts et al.,
Ann. Rev. Pharmacol. Toxicol. 17: 97 (1977), and include
high activity at physiological pH and no requirement for
exogenous cofactors. The histidine ammonia lyase isolated
from a bacterium of the family Corynebacteriaceae, herein 40
denoted as "HAL," has been partially characterized by
Roberts et al., *Cancer Treat. Rep.* 63: 1045 (1979). HAL
demonstrates a broad useful pH range with approximately
75% of activity being retained at pH 7.2. The plasma
half-life of HAL in mice is eight hours. The usefulness of 45
this enzyme for histidine depletion in vivo is evident from
the observation that single intraperitoneal injections of 400
IU/kg effectively depleted plasma histidine in mice for up to
24 hours. However, the Corynebacteriaceae HAL which
Roberts et al. described was not in purified form. As a result,
many of the therapeutically beneficial properties associated
with this HAL were unknown.

Histidine ammonia lyases have been isolated from several
bacterial, animal, mammalian and plant sources. Shibatani et
al., *Eur. J. Biochem.* 55: 263–269 (1975). Km values of these 55
enzymes range between 1 and 20 mM. Shibatani (1975),
supra; Wu et al., *Gene.* 115: 19–25 (1992); Jack et al.,
Leukemia Research, 7: 421–429 (1983); Khanna and Chang,
Int'l J. Artificial Organs 13: 189–195 (1990). Genes coding
for histidine ammonia lyases have been cloned from a 60
number of organisms (Consevage, M. W. and A. T. Phillips.
1990. *Journal of Bacteriology.* 172 (5): 2224–2229; Oda, M.
Sugishita, A. and K. Furukawa. 1988. *J. Bacteriology.*
170(7): 3199–3205; Wu, P. C., Kroening, T. A., White, P. J.
and Kendrick, K. E. 1992. *J. Bacteriology.* 174(5): 65
1647–1655; Taylor, R. G., Lambert, M. A., Sexsmith, E.,
Sadler, S. J., Ray, P. N., Mahuran, D. J. and McInnes, R. R.

1990. *J. Biol. Chem.* 265(30): 18192–18199). Biochemical
characterization has shown that most histidine ammonia
lyases are inhibited by EDTA and thiol reagents (Shibatani,
T., Kakimoto, T. and I. Chibata. 1975. *Eur. J. Biochem.* 55:
263–269; Okamura, H., Nishida, T. and H. Nakajawa. 1974.
J. Biochem. 75: 139–152). A bioactive histidine ammonia
lyase from a bacterium identified as *Kurthia* species was
described by Jack, et al. in 1983 (Jack, G. W., Wiblin, C. N.
and P. C. McMahon. 1983. *Leukemia Research*, 7(3):
421–429.) The *Kurthia* species histidine ammonia lyase was
reported to have a K_m of 1.25 mM with a half-life of 6–7
hours in mice. Chemical modification of the *Kurthia* histi-
dine ammonia lyase did not increase the biological half-life
of this enzyme. However, while HAL isolated from Coryne-
bacteriaceae was effective in reducing ascites tumors in mice
with high cell challenge (10^7 cells per mouse), the histidine
ammonia lyase isolated from *Kurthia* was reported to be
effective only at low tumor cell challenge levels (10^3 to 10^5
cells per mouse).

L-histidinol is an analog of histidine that is capable of
altering histidine metabolism. Alteration of histidine
metabolism by L-histidinol has provided therapeutic benefit.
Histidine is required for several cellular processes, including
protein synthesis and formation of histamine, both of which
are required for tumor growth (Watanabe, et al, 1982.
Biochem. and Biophys. Res. Comm. 109:478–485; Bart-
holeyns and Bouclier. 1982. *Cancer Res.* 44:639–645;
Hakii, et al, 1986. *J. Cancer Res. and Clin. Oncol.*
111:177–181). Histidine is a direct precursor of histamine
and is converted to histamine by the enzyme histidine
decarboxylase (HDC). L-histidinol interferes with this con-
version by inhibiting HDC. Therefore, L-histidinol can act
therapeutically by inhibiting HDC, which is induced by
strong tumor promoting phorbol esters (Mitra, et al, 1993. *J.*
Cellular Physiol., 156:348–357). L-histidinol possesses
some anti-tumor activity, as well as an ability to reverse
resistance of certain tumor cell lines to some antineoplastic
compounds (Stolfi, R. L. and Martin, D. S. 1990.
Chemotherapy, 36 (6): 435–440; Warrington, R. C., Fang W.
D. and L. U. Zhang, 1996. *Anticancer Research* 16 (6B):
3641–3646; Warrington, R. C. and Fang W. D. 1989. *Jour-*
nal of the National Cancer Institute. 81 (10): 798–803).
L-histidinol is also able to enhance the efficacy of certain
anti-cancer drugs, when both are administered to a patient
simultaneously. (Warrington, R. C. and W. D. Fang. 1991.
Anticancer Research, 11 (5): 1869–1874; Warrington, R. C.,
Cheng, I. And W. D. Fang. 1994. *Anticancer Research*, 14
(2A): 367–372; Warrington, R. C., Cheng, I., Zhang, L. and
W. D. Fang. 1993. *Anticancer Research*, 13 (6A):
2107–2112; Warrington, R. C. 1992. *Biochemistry and Cell*
Biology, 70 (5): 365–375; Zaharko, D., Plowman, J., Waud,
W., Dykes, D. and L. Malspeis. 1992. *Cancer Research*, 52
(13): 3604–3609). For example, the therapeutic index of
chemotherapeutic agents is increased by combining treat-
ment with L-histidinol, since L-histidinol reduces the tox-
icity of normal chemotherapeutic agents to normal cells but
not to cancer cells (Warrington, R. C., Fang, W. D., Zhang,
L. Shieh, M. and M. H. Saier, Jr. 1996. *Anticancer Research*,
16 (6B): 3635–3639; Warrington, R. C., Fang W. D., Zhang,
L., Shieh, M. and M. H. Saier, Jr. 1996. *Anticancer*
Research, 16 (6B): 3629–3633; Badary, O. A., Nagi, M. N.,
Al-Sawaf, H. A., Al-Harbi, M., and A. M. Al-Bekairia. 1997.
Nephron, 77 (4): 435–439; Al-Shabanah, O. A., Badary, O.
A., Al-Gharably, N. M. and H. A. Al-Sawaf. 1998. *Phar-*
macological Research, 38 (3): 225–230; Badary, O. A. 1999.
Experimental Nephrology, 7 (4): 323–327).

In theory, the use of L-histidinol with a histidine ammonia
lyase offers a therapeutic approach to depleting serum

histamine and lowering histidine levels. L-histidinol has limited usefulness as a single agent due to its low half-life (Zaharko, D., Plowman, J., Ward, W., Dykes, D., and L. Malspeis, 1992. *Cancer Research*. 52: 3604–3609) and its mode of action as a competitive inhibitor. Accordingly, L-histidinol must be present in very high concentrations in order to competitively inhibit cellular processes involving histidine. Reduced histidine levels would enhance the effectiveness of L-histidinol, by allowing cells to uptake the L-histidinol more readily.

Nevertheless, a histidine ammonia lyase suitable for combination therapy with a histidine analog, such as L-histidinol, must have the additional property of not being inhibited by L-histidinol. One prevalent characteristic of all known isolated histidine ammonia lyases is their inhibition in the presence of a histidine analog, like histidinol. For example, histidine ammonia lyases isolated from bacteria such as *Achromobacter liquidum* and *Streptomyces griseus* are inhibited by L-histidinol and L-histidinol phosphate, respectively, with a K_i of 4.58 and 0.27 mM, respectively (Shibatani, T. et al. 1975. *Eur. J. Biochem.* 55: 263–269; Wu, P. C. et al. 1995. *Gene*. 115(1–2): 19–25).

Due to their enzymatic inhibition by histidinol, previously described histidine ammonia lyases have not been suitable candidates for use in combination therapies with these histidine analogs for treating pathologies such as cancer. Accordingly, there is a present and unmet need for a histidine ammonia lyase that possesses the relevant properties associated with previously isolated histidine ammonia lyases, yet maintains the ability to deplete histidine in the presence of L-histidinol.

In addition to cancer, viral diseases such as Human Respiratory Syncytial Virus (RSV), Herpes Simplex Virus (HSV) and Human Immunodeficiency Virus (HIV), infect millions worldwide and cause major health problems. RSV, a common cause of winter outbreaks of acute respiratory disease, in 1998 resulted in 90,000 hospitalizations and 4,500 deaths and is the largest cause of lower respiratory tract disease among infants and young children in the United States (CDC. 1997. *MMWR*. 46(49); 1163–1165). Herpes Simplex Virus infects an even larger portion of the population. The Centers for Disease Control estimated that in 1998, 45 million people ages 12 and older, or one out of five of total adolescent and adult population, was infected with the Herpes Simplex Virus. The Joint United Nation Programme on HIV/AIDS (UNAIDS) estimates that worldwide 33.6 million persons are infected with HIV/AIDS and 2.6 million people died in 1999 from this disease.

Human infectious viruses vary widely in the way they enter cells, replicate inside the cells, and subsequently get released from infected cells. RNA viruses have single- or double-stranded RNA as their genomes, which are naked or enveloped. The RNA strand can be either in a positive or negative form. RNA viruses enter the cell, make copies of their RNA genome, and direct the synthesis of messenger RNA to code for structural and regulatory proteins. Finally, the genome is assembled with structural proteins and the virus is released. DNA viruses have single- or double-stranded DNA genomes that can be either non-enveloped or enveloped. Retroviruses are also RNA viruses but they involve DNA in their replication process. Thus, each virus is unique in its infection and multiplication process.

One common theme in viral replication is the ability of a virus to utilize the human cellular machinery for its multiplication. This makes drug development against viruses very difficult. In the past, antiviral therapy has focused on devel-

opment of appropriate vaccines or inhibiting unique processes in viral replication. This often renders such therapy very specific for a type or subtype of viruses. Currently, vaccines are the main line of defense against viruses. Vaccines are developed specifically for each virus type and subtype, and are useful only against that particular virus type/subtype.

Therapies also have been developed that take advantage of unique processes in viral replication. For example, reverse transcriptase is unique to retroviruses. Nucleotide analogs and non-nucleotide reverse transcriptase inhibitors have been developed that inhibit reverse transcriptase without affecting other polymerases. However, such therapy is limited to combating only retroviruses. Yet another approach that targets a unique viral replication process is the use of protease inhibitors against HIV. But since these inhibitors target a specific enzyme, HIV protease, they cannot be effective against a wide range of viruses. Yet another example of a virus-specific therapy is the use of the antiviral compound ganciclovir, which is effective against Herpes Simplex Virus. Ganciclovir is specifically cytotoxic to herpes infected cells. Although ganciclovir therapy may be beneficial to combating the Herpes Simplex Virus, it has limited or no application for treating other viruses.

Accordingly, there is a great need for a therapeutic agent that can be effective against a broad spectrum of viruses. There has been no indication heretofore that a peptide having a histidine ammonia lyase activity could effectively treat infectious viral agents. Thus, a substantial therapeutic and market potential exists for a histidine ammonia lyase that is effective against infectious viral agents.

SUMMARY OF THE INVENTION

Accordingly, it is an object of the invention to provide a purified polypeptide having a histidine ammonia lyase activity that is not substantially inhibited by a histidine analog, such as histidinol.

It is a further object of the invention to provide a method for treating cancer, using a histidine analog, such as histidinol and a purified polypeptide having a histidine ammonia lyase activity that is not substantially inhibited by such compounds.

It is still a further object of the invention to provide a method for treating a viral infection, using a purified polypeptide having a histidine ammonia lyase activity.

These and other objects of the invention will become apparent to one of ordinary skill in the art upon reading the present application.

In one aspect, the invention provides an isolated polypeptide having histidine ammonia lyase activity, wherein the histidine ammonia lyase activity is not substantially decreased in the presence of a histidine analog such as histidinol. The invention also provides a polypeptide having the preceding characteristics, which comprises a peptide sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, and SEQ ID NO: 6. The invention also provides a polypeptide having the preceding characteristics, which comprises a peptide sequence selected from the group consisting of SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, and SEQ ID NO: 11. The invention further provides a method for PEGylating an isolated polypeptide having the preceding characteristics, comprising reacting a PEG with the polypeptide.

In a methodological aspect, the invention provides a method for treating a patient suffering from a viral disorder,

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comprising administering to a patient suffering from a viral infection a therapeutic amount of a polypeptide having histidine ammonia lyase activity.

The invention further provides a method for treating a patient suffering from a cancer, comprising administering to the patient suffering from the cancer 1) a therapeutic amount of an isolated polypeptide having histidine ammonia lyase activity, wherein said histidine ammonia lyase activity is not substantially decreased in the presence of a histidine analog such as histidinol and 2) a therapeutic amount of a histidine analog.

In a further methodological approach, the invention provides a method for treating disease, comprising administering to a patient 1) a therapeutically effective amount of a polypeptide having histidine ammonia lyase activity and 2) administering to the patient a therapeutically effective amount of a chemotherapeutic agent or a retroviral vector. Consistent with this methodology, the invention provides a method for treating disease according to the previous method, wherein upon the administration of the polypeptide, non-diseased cells of the patient enter a reversible quiescent state.

The invention also provides a method for delivering an immunosuppressant to a patient, comprising: 1) administering to a patient a therapeutically effective amount of a polypeptide having histidine ammonia lyase activity, wherein the polypeptide generates trans-urocanic acid (t-UA) in vivo; and 2) subjecting the patient to an irradiating agent, wherein the irradiating agent causes the photoisomerization of t-UA to its cis isomer (c-UA), and wherein said cis isomer comprises an immunosuppressive property.

The present invention also includes an isolated DNA sequence comprising SEQ ID NO: 7, as well as an expression vector comprising SEQ ID NO: 7. In addition, the invention provides a method for treating a patient comprising constructing an expression vector comprising SEQ ID NO: 7 and introducing the expression vector into the patient.

The present invention further includes an isolated DNA sequence comprising SEQ ID NO: 12, as well as an expression vector comprising SEQ ID NO: 12. In addition, the invention provides a method for treating a patient comprising constructing an expression vector comprising SEQ ID NO: 12 and introducing the expression vector into the patient.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 shows the restriction pattern of the HAL coding region cut with selected enzymes.

FIG. 2 lists the experimentally derived peptide sequences of HAL (portion of SEQ ID NO: 3—n-terminal— and SEQ ID NOS 32–33—internal).

FIG. 3 depicts the SphI digestion pattern of HAL gene showing oligonucleotide and subclones.

FIG. 4 depicts a histidine ammonia lyase overexpressing plasmid.

FIG. 5 is an SDS-PAGE illustration, showing expression of HAL in *E. coli*. 30 μ g samples were loaded onto a 10% SDS-PAGE gel. Lane 1: Sample taken at 1 hour following induction. Lane 2: Sample taken at 2 hours following induction. Lane 3: Sample taken at 3 hours following induction. Lane 4: Sample taken at 4 hour following induction.

FIG. 6 is a picture of the SDS-PAGE showing purification of HAL from *E. coli*. Lanes 1 and 4 contain 10 and 20 μ g respectively of crude extract. Lanes 2 and 5 contain 5 and 10

6

μ g respectively of phenyl sepharose pooled fractions. Lanes 3 and 6 contain 5 and 10 μ g respectively of Q-sepharose pooled fractions.

FIG. 7 is a graph depicting the effect of temperature on HAL.

FIG. 8 is a graph depicting the effect of pH on HAL.

FIG. 9 is a chart illustrating the effect of HAL and Histidinol on HSV. Lane 1: Control. Lane 2: HAL alone (0.003 U/ml) Lane 3: L-histidinol alone (0.5 mM). Lane 4: HAL and L-histidinol (0.003 U/ml and 0.5 mM respectively).

FIG. 10 depicts the effectiveness of L-histidinol as a single agent. Lane 1: Control. Lane 2: L-histidinol (0.1 mM). Lane 3: L-histidinol (0.5 mM). Lane 4: L-histidinol (1.0 mM). Lane 5: L-histidinol (1.5 mM). Lane 6: L-histidinol 3.0 mM).

FIG. 11 depicts the effect of HAL and Histidinol on RSV. Lane 1: Control. Lane 2: HAL alone (0.005 U/ml). Lane 3: L-histidinol alone (3.0 mM). Lane 4: HAL and L-histidinol (0.005 U/ml and 3.0 mM respectively).

FIG. 12 depicts the effect of HAL on RMuLV. Lane 1: Control. Lane 2: HAL (0.001 U/ml). Lane 3: HAL (0.002 U/ml). Lane 4: HAL (0.004 U/ml).

FIG. 13 (SEQ ID NOS 34–42, respectively, in order of appearance) illustrates a first peptide sequence pileup of HAL from various bacteria, including Corynebacteriaceae, *B. subtilis*, *S. griseus*, *P. putida*.

FIG. 14 (SEQ ID NOS 43–64, respectively, in order of appearance) is a second peptide sequence pileup of HAL from various bacteria, including Corynebacteriaceae, *S. griseus*, and *D. radiodurans*.

FIG. 15 (SEQ ID NOS 65–66, respectively, in order of appearance) is a comparison between the amino acid sequence of *S. griseus* (“STRG”) and Corynebacteriaceae (“HAL”); positions of an amino acid identity are delineated by “*”.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

The present inventors have discovered that certain polypeptides, known as histidase or histidine ammonia lyases, can decrease serum histidine levels and induce accumulation of urocanic acid, and yet are not inhibited by analogs of histidine, such as histidinol. By virtue of this discovery, a bioactive histidine ammonia lyase according to the invention can be used to treat allergic reactions and pathologies characterized by increased levels of or need for histidine and/or histamine, such as cancer and infectious viruses.

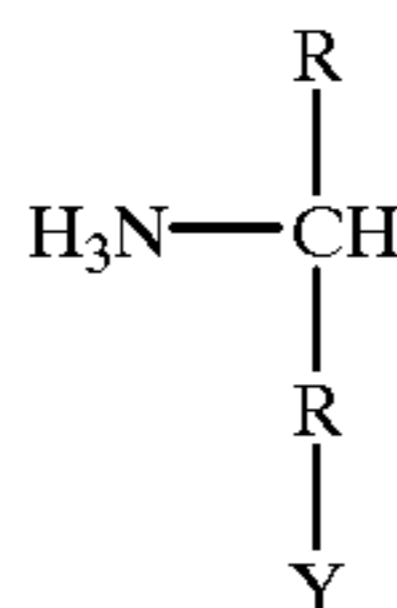
The Inventive Polypeptides and Nucleic Acids

In one of its aspects, the present invention provides a polypeptide, commonly known as “histidase” or “histidine ammonia lyase,” that depletes L-histidine serum levels, in turn producing urocanic acid—a beneficial by-product of histidine breakdown. A histidine ammonia lyase (EC 4.3.1.3) catalyzes the nonoxidative elimination of the alpha-amino group of histidine. Although L-histidinol is able to alter histidine metabolism, alteration of histidine metabolism via depletion of histidine with a histidine ammonia lyase would provide similar therapeutic benefits, yet would do so in an even more effective and potentially less toxic manner than L-histidinol. An additional advantage for treatment with histidine ammonia lyase is that one of the products of its action, urocanic acid, promises to have protective and beneficial effects on the immune system, as reported by Noonan et al., *Immunol. Today* 13: 250–254 (1992).

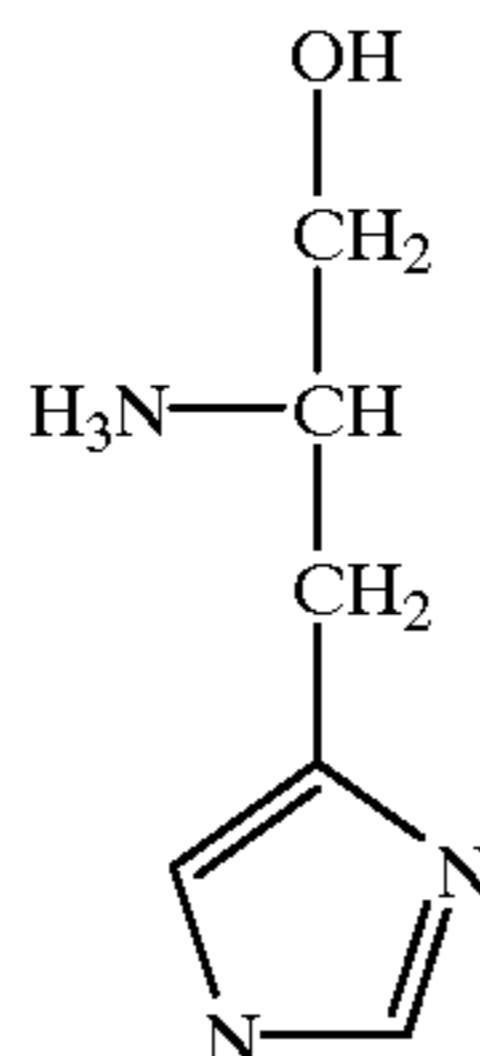
In another aspect, the invention contemplates a polypeptide that is able to retain its histidine ammonia lyase activity in the presence of a histidine analog, like histidinol. As defined herein, a “histidine analog” refers to histidine variants, like histidinol, including therapeutic salts thereof. Histidinol, as a representative histidine analog, possesses many beneficial therapeutic uses, including the ability to inhibit the production of histamine from histidine. Histidinol is also able to alter protein synthesis pathways, by causing deacylation of histidyl tRNA. Because the histidine ammonia lyase activity of a polypeptide according to this invention is not substantially decreased in the presence of a histidine analog, like histidinol, it is uniquely suitable among all other known histidine ammonia lyases for combination therapy with such compounds.

Nucleic acids encoding the inventive peptides also are contemplated, as are conservative variants thereof, in accordance with the “sequence identity” discussion below. The inventive nucleic acids are, of course, useful in preparing the inventive proteins by recombinant means and in implementing gene therapy treatments analogous to the protein-based treatments, discussed below.

Histidine analogs, according to the invention, include compounds of the following structure:



wherein each R is independently a 1-, 2- or 3-carbon alkyl, a 2- to 3-carbon alkene, or a 2- to 3-carbon alkyne, wherein each R independently is optionally substituted one or members of the group consisting of —OH, —SH and =O; and Y is a 5- or 6-membered heterocyclic ring, having one or two hetero atoms selected from the group consisting of N, S and O, including esters and therapeutically effective salts thereof. In some preferred analogs Y is a five-membered ring, having one or two N hetero atoms and in more preferred compounds Y is an imidazole moiety. In certain preferred compounds N is 1. R specifically may be a 1-carbon alkyl. Representative esters include phosphoric acid esters and carboxylic acid esters (especially C1–3). Analogs can include histidinol, histidinal, imidazole glycerol phosphate, imidazole acetol phosphate, and histidinol phosphate. Histidinol has the following structure:



The polypeptides of the present invention have a molecular structure that confers the functional characteristics described herein. In a preferred embodiment, the region is conserved that corresponds to the active site, denoted by SEQ ID NO: 1. Accordingly, the peptide sequences delineated by SEQ ID NOS: 2, 3, 4, and 5 are encompassed by the invention because they conserve the active site of the

novel polypeptide. Likewise, SEQ ID NOS: 8, 9, and 10 conserve the active site of the novel polypeptide and, accordingly, are contemplated by the invention.

Within the present invention, moreover, are molecules that do not contain the active site, but are variants of the aforementioned peptides by virtue of one or more conservative substitution, such as cysteine for serine—both of which are sulfur-containing amino acids—that maintain histidine ammonia lyase activity in the presence of a histidinol analog. A “conservative substitution” may be made, for instance, on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved.

Thus, the overall structure and composition of inventive polypeptides are important only insofar as they confer the appropriate functional characteristics, i.e., histidine-depleting and relative resistance to a histidine analog, such as histidinol. Given the properties of the individual amino acids comprising the disclosed protein products, some rational substitutions will be recognized by the skilled worker. For example: (a) nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; (b) polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; (c) positively charged (basic) amino acids include arginine, lysine, and histidine; and (d) negatively charged (acidic) amino acids include aspartic acid and glutamic acid. Substitutions typically may be made within groups (a)–(d). In addition, glycine and proline may be substituted for one another based on their ability to disrupt α -helices. Similarly, certain amino acids, such as alanine, cysteine, leucine, methionine, glutamic acid, glutamine, histidine and lysine are more commonly found in α -helices; while valine, isoleucine, phenylalanine, tyrosine, tryptophan and threonine are more commonly found in β -pleated sheets. Glycine, serine, aspartic acid, asparagine, and proline are commonly found in turns. Some preferred substitutions may be made among the following groups: (i) S and T; (ii) P and G; and (iii) A, V, L and I. Given the known genetic code, and recombinant and synthetic DNA techniques, the skilled scientist can readily construct DNAs encoding the conservative amino acid variants.

In general, both the DNA and protein molecules of the invention can be defined with reference to “sequence identity.” Some molecules have at least 60% identity. Preferred molecules are those having at least about 65% sequence identity, more preferably at least 65% or 70% sequence identity. Other preferred molecules have at least 80%, more preferably at least 80% or 85%, sequence identity. Particularly preferred molecules have at least about 90% sequence identity, more preferably at least 90% sequence identity. Most preferred molecules have at least about 95%, more preferably at least 95%, sequence identity. As used herein, two nucleic acid molecules or proteins are said to “share significant sequence identity” if the two contain regions which possess greater than 85% sequence (amino acid or nucleic acid) identity.

“Sequence identity” is defined herein with reference the Blast 2 algorithm, which is available at the NCBI (<http://www.ncbi.nlm.nih.gov/BLAST>), using default parameters. References pertaining to this algorithm include: those found at http://www.ncbi.nlm.nih.gov/BLAST/blast_references.html; Altschul, S. F., Gish, W., Miller, W., Myers, E. W. & Lipman, D. J. 1990. *J. Mol. Biol.* 215:403–410; Gish, W. & States, D. J. 1993. *Nature Genet.* 3:266–272; Madden, T. L., Tatusov, R. L. & Zhang, J. 1996. *Meth. Enzymol.* 266:131–141; Altschul, S. F., Madden, T. L., Sch

ffer, A. A., Zhang, J., Zhang, Z., Miller, W. & Lipman, D. J. 1997. *Nucleic Acids Res.* 25:3389–3402; and Zhang, J. & Madden, T. L. 1997. *Genome Res.* 7:649–656.

To this end, SEQ ID NO: 6, for example, delineates sequence variations that are contemplated by the invention. The amino acid positions not represented by “X” represent 1) highly conserved regions among known histidine ammonia lyases (see e.g., FIG. 15), as well as 2) amino acids that are unique to the polypeptide isolated from Corynebacteriaceae. Regions corresponding to the absence of an amino acid are denoted by “-”, shown in FIG. 14. Amino acid positions delineated by “X” represent regions where the amino acid can vary without departing from the invention. According to SEQ ID NO: 6, the amino acids represented by “X” can be an amino acid that is present in the corresponding position of any other histidine ammonia lyase. For instance, FIG. 14 denotes Alanine at position 14 of the HAL isolated from Corynebacteriaceae. In histidine ammonia lyases isolated from those species depicted in FIG. 14, the amino acid at the position corresponding to position 14 in Corynebacteriaceae are: threonine, alanine, valine, leucine, asparagine, aspartic acid, and proline, as shown in FIG. 14. Accordingly, position 14 of the polypeptide contemplated by the invention can be represented by any one of these amino acids. To further illustrate the contemplated variation, the amino acid corresponding to position 241 can be Phenylalanine, leucine, tyrosine, alanine, or cysteine.

The Following Legend is used to describe the species associated with the peptides disclosed in FIG. 14.

983831	:	HAL
	CAC21618	: <i>Streptomyces coelicolor</i>
	HUTH_STRGR	: <i>Streptomyces griseus</i>
	HUTH_DEIRA	: <i>Deinococcus radiodurans</i>
4	BAB16159	: <i>Agrobacterium rhizogenes</i>
5	Q9KWE4	: <i>Agrobacterium rhizogenes</i>
	HUTH_BACSU	: <i>Bacillus subtilis</i>
7	Q9KSQ4	: <i>Vibrio cholerae</i>
8	Q9HU85	: <i>Pseudomonas aeruginosa</i>
9	Q9KBE6	: <i>Bacillus halodurans</i>
	HUTH_PSEPU	: <i>Pseudomonas putida</i>
	HUTH_RHIME	: <i>Rhizobium meliloti</i>
12	Q9HU90	: <i>Pseudomonas aeruginosa</i>
	HUTH_HUMAN	: Human
	HUTH_CAEEL	: <i>Caenorhabditis elegans</i>
15	Q9HLL6	: <i>Thermoplasma acidophilum</i>
	HUTH_MOUSE	: Mouse
17	BAB29407	: <i>Mus musculus</i> (Mouse)
18	HUTH_RAT	: Rat
18	AAG53586	: uncultured bacterium pCosAS1
20	Q9KKEO	: <i>Rhizobium meliloti</i>
21	Q9HQD5	: <i>Halobacterium sp</i>

A further example, as shown by SEQ ID NO: 11, delineates other contemplated peptides, which can be formulated by referencing the histidine ammonia lyases set forth in FIG. 13. As in SEQ ID NO: 6, the amino acid positions not represented by “X” represent 1) highly conserved regions among known histidine ammonia lyases, as well as 2) amino acids that are unique to the polypeptide isolated from Corynebacteriaceae. Regions that may correspond to the absence of an amino acid are denoted by “-”, shown in FIG. 13. Amino acid positions delineated by “X” represent regions where the amino acid can vary without departing from the invention. The amino acids represented by “X” can be an amino acid that is present in the corresponding position of any other histidine ammonia lyase. For instance, FIG. 13 denotes Threonine at position 8 of the HAL isolated from Corynebacteriaceae. In histidine ammonia lyases isolated from other species, the amino acid at the position

corresponding to position 8 in Corynebacteriaceae are threonine, isoleucine, alanine, glutamate, and valine, also shown in FIG. 13. Accordingly, position 8 of the polypeptide contemplated by the invention can be represented by any one of these amino acids. To further illustrate the contemplated variation, the amino acid corresponding to position 307 can be alanine, aspartate, glycine, glutamate, or arginine.

In addition to having varying peptide sequences, the polypeptides contemplated by the invention can possess varying molecular weights, without departing from the invention, so long as one or more of the novel properties, as disclosed herein, are maintained. Accordingly, a polypeptide can have a monomeric molecular weight between about 30,000 to 67,000 daltons. More preferably, the monomeric molecular weight is between about 45,000 and 60,000 daltons. It is most preferred that the monomeric molecular weight is about 56,000 daltons.

Therapeutic Compositions

The proteins of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby the inventive molecules, or their functional derivatives, are combined in a mixture with a pharmaceutically acceptable carrier vehicle. Suitable vehicles and their formulation, inclusive of other human proteins, e.g., human serum albumin, are described, for example, in *Remington's Pharmaceutical Sciences* (16th ed., Osol, A., Ed., Mack, Easton Pa. (1980)). In order to form a pharmaceutically acceptable composition suitable for effective administration, such compositions will contain an effective amount of one or more of the proteins of the present invention, together with a suitable amount of carrier vehicle.

Pharmaceutical compositions for use in accordance with the present invention may be formulated in conventional manner using one or more physiologically acceptable carriers or excipients. Thus, the inventive polypeptides and their physiologically acceptable salts and solvate may be formulated for administration by inhalation or insufflation (either through the mouth or the nose) or oral, buccal, parenteral or rectal administration.

For oral administration, the pharmaceutical compositions may take the form of, for example, tablets or capsules prepared by conventional means with pharmaceutically acceptable excipients such as binding agents (e.g., pregelatinised maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose); fillers (e.g., lactose, microcrystalline cellulose or calcium hydrogen phosphate); lubricants (e.g., magnesium stearate, talc or silica); disintegrants (e.g., potato starch or sodium starch glycolate); or wetting agents (e.g., sodium lauryl sulfate). The tablets may be coated by methods well known in the art. Liquid preparations for oral administration may take the form of, for example, solutions, syrups or suspensions, or they may be presented as a dry product for constitution with water or other suitable vehicle before use. Such liquid preparations may be prepared by conventional means with pharmaceutically acceptable additives such as suspending agents (e.g., sorbitol syrup, cellulose derivatives or hydrogenated edible fats); emulsifying agents (e.g., lecithin or acacia); non-aqueous vehicles (e.g., almond oil, oily esters, ethyl alcohol or fractionated vegetable oils); and preservatives (e.g., methyl or propyl-p-hydroxybenzoates or sorbic acid). The preparations may also contain buffer salts, flavoring, coloring and sweetening agents as appropriate.

Preparations for oral administration may be suitably formulated to give controlled release of the active compound.

For buccal administration the composition may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the novel polypeptide for use according to the present invention is conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g. gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch.

The novel polypeptide may be formulated for parenteral administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, e.g., containing conventional suppository bases such as cocoa butter or other glycerides.

In addition to the formulations described previously, the novel polypeptide may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

The compositions may, if desired, be presented in a pack or dispenser device which contain one or more unit dosage forms containing the active ingredient. The pack may for example comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration.

Methods of the Invention:

Therapeutic Rationale

Viral Fighting Properties

In one embodiment, the inventive polypeptides possess hitherto unknown uses for treating human infectious viruses, including DNA and RNA viruses. It has been discovered by the present inventors the novel polypeptides are surprisingly potent inhibitors of RNA, DNA and retroviruses viruses. Histidine ammonia lyase therapy by itself and in combination with histidinol is effective against these three main groups of viruses. The unique broad-spectrum antiviral activity of HAL is a highly desirable characteristic for an antiviral agent.

Specific viruses that can be treated according to the invention include, but are not limited to, human Respiratory Syncytial Virus (RSV), Herpes Simplex Virus (HSV) and Human Immunodeficiency Virus (HIV). The latter virus can be treated in accordance with the present invention, based on the observation that inventive polypeptide was able to inhibit viral replication in the Rauscher Murine Leukemia Virus, a model virus for HIV. Other treatable viruses include the following closely related viruses.

Respiratory syncytial virus belongs to the family Paramyxoviridae. The other human infectious viruses belonging to the family Paramyxoviridae include: Parainfluenza 1, 2, 3, 4 viruses which cause upper respiratory disease, bronchitis/bronchiolitis, pneumonia; mumps virus, and measles virus. The family Paramyxoviridae is very closely related to Rhabdoviridae and Filoviridae because the viruses belonging to these families contain a single-stranded RNA (negative sense) genome which is non-segmented and enveloped. Human infectious viruses belonging to Rhabdoviridae are vesicular stomatitis-Indiana, New Jersey, coccal viruses, chandipura virus, Piry virus, Isfahan virus, rabies virus, Mokola virus, and Duvenhage virus. Human infectious viruses belonging to the family Filoviridae include Marburg and Ebola viruses. More broadly, Respiratory Syncytial Virus is an RNA virus.

Other RNA viruses that cause human infections include the following: polioviruses 1, 2, and 3; coxsackieviruses B1-B6; human echoviruses 1-9, 11-27, and 29-34; human enteroviruses 1-113; Norwalk virus and similar viruses that belong to the family Caliciviruses that cause gastroenteritis in humans; eastern equine encephalitis virus; western equine encephalitis virus; Venezuelan equine encephalitis virus; chikungunya virus; O'nyong-nyong virus; Ross River virus; Mayaravirus; rubella virus; yellow fever virus; dengue viruses; Western Nile virus; St. Louis encephalitis virus; Japanese encephalitis virus; Murray Valley encephalitis virus; Rocio virus; tick-borne encephalitis viruses; human coronaviruses 229-E and OC43; upper respiratory tract infection, probably pneumonia and possibly gastroenteritis; influenza A, B, and C viruses; Bunyamwera virus; Bwamba virus; Oriboca virus; Oropouche virus; Gwama virus; California encephalitis virus; LaCrosse virus; Tahyna virus; Sandfly fever-Naples virus; Crimean-Congo hemorrhagic fever virus; Hantaan virus (Korean hemorrhagic fever, hemorrhagic fever with renal syndrome, nephropalithia epidemica); lymphocytic choriomeningitis (LCM) virus; Lassa virus; Machupa virus (Bolivian hemorrhagic fever); Junin virus (Argentine hemorrhagic fever); reovirus 1, 2, and 3; Orungo virus (febrile illness in Nigeria and Uganda); Kemerovo virus (febrile illness in Russia and Egypt); human rotaviruses, Colorado tick fever virus.

Rauscher Murine Leukemia virus belongs to the family Retroviridae. Viruses that belong to this family have a single-stranded (positive sense), non-segmented enveloped genome, but they involve a DNA step in replication. Human infectious viruses belonging to this family include type C oncoviruses such as human T-lymphotropic virus 1 (HTLV-I, adult T-cell leukemia) and human T-lymphotropic virus 2 (HTLV-II, possibly associated with hairy-cell leukemia), human immunodeficiency viruses 1 and 2 (HIV 1 and HIV 2) that cause acquired immunodeficiency syndrome (AIDS) and other viruses, related to HIV 1 and HIV 2, which cause AIDS-like disease.

Herpes Simplex Virus belongs to the family Herpesviridae. Viruses belonging to the family Herpesviridae have a double-stranded enveloped genome, a property that they share with viruses belonging to the families Poxviridae and Iridoviridae. Human infectious viruses belonging to the family Herpesviridae include Herpes Simplex Viruses 1 and 2, cercopithecine, herpesvirus 1 (B-virus), varicella-Zoster virus, human cytomegalovirus, EB virus, and human herpesvirus 6. Human infectious viruses belonging to Poxviridae include variola virus (smallpox, alastrim), vaccinia virus, monkeypox virus, cowpox virus, orf virus (contagious pustular dermatitis), pseudo-cowpox (milker's nodule) virus, yabapox virus, tanapox virus, and molluscum contagiosum

virus. More broadly, Herpes Simplex Virus is a DNA virus and other human infectious viruses in this category are hepatitis B virus; human parvovirus B-19, parvovirus RA-1, and other parvoviruses that cause gastroenteritis; human papillomaviruses (HPV) 1–48); polyomaviruses such as JC, SV40 and BK; and Adenoviruses such as Mastadenovirus h1–h49.

Polypeptides that have a histidase activity are able to combat viruses by inhibiting viral replication, for example, in the absence of a histidine analog. However, a greater therapeutic benefit is achieved, when treating viruses, if the polypeptides of the invention are employed in conjunction with a histidine analog, like histidinol, as shown in Example 11. In fact, a synergistic effect is observed when HAL- and histidine analog-directed therapies are combined, also shown in Example 11. Accordingly, the invention contemplates polypeptides that can be used to treat infectious viruses by virtue of the polypeptide's histidine depleting activity, either alone or in combination with a histidine analog.

Cancer Fighting Properties

In another aspect, the inventive polypeptide is able to function as an anticancer agent. In vitro, the polypeptides of the invention are effective in controlling the growth of a variety of human tumors. For example, the growth of different prostate and ovarian cancer cell lines has been inhibited by the inventive polypeptides, as shown in Example 12.

By virtue of their anti-carcinogenic activity in vitro, the polypeptides of the invention can also be used to inhibit malignant tumor proliferation in vivo. In addition, any of the novel polypeptides are a suitable candidate for an anticancer agent that can be used in combination therapy with other anticancer agents, as described below. In particular, the polypeptides of the present invention can be administered to a patient in the presence of a histidine analog, like histidinol, due to the novel polypeptides' ability to retain histidine ammonia lyase activity in the presence of such compounds.

There are numerous types of cancers that can be treated according to the invention, including prostate and ovarian cancer, and glioblastomas. Other types of cancers that may be treated include: chronic and acute leukemia, cancer of the bone, brain, breast cartilage, cervix, esophagus, kidney, larynx, liver, lung, pancreas, and uterus. In addition, the polypeptides of the invention may be used to combat Hodgkin's Disease, lymphoma, melanoma, multiple myeloma, colo-rectal, and testicular cancer.

Quiescent-inducing Properties

It has been discovered that incubation in histidine-deficient medium has been able to cause non-transformed mammalian cells to enter a reversible inactive, or "quiescent," state at a specific point during the cell cycle, called the "restriction point." Newman et al. 1983. *Anticancer Research*. 43:4703. This quiescent state is characterized by an absence of DNA synthesis and reduced rates of ribosomal RNA and protein synthesis. These and a series of other metabolic events associated with growth quiescence are reversible, and have been termed the "negative pleiotypic response." In contrast to the reversible arrest of normal cells by nutritional manipulations, transformed cell lines seem to have lost their ability to stop proliferation at the restriction point, as reported by Pardee et al. *Annual Rev. Biochem.* 47:715–750 (1974); and Pardee, *Proc. Natl. Acad. Sci. U.S.A.* 71: 1286–1290 (1974) and Newman et al., (1983), supra.

This fundamental difference between normal and malignant cells can be exploited to selectively kill transformed

cells under conditions that leave normal cells intact. For example, chemotherapeutic drugs function preferentially against proliferating cells, with no significant capacity to discriminate between cycling normal and cycling tumor tissues. Previously, Newman et al., *Anticancer Res.* 43: 4703 (1983) were able to drive a cell line (BALB/3T3) into a quiescent state by incubating the cell line in a histidine-deficient medium. This methodology protected the cells from the lethal effects of Methotrexate. Warrington, *Anticancer Res.* 6: 451 (1986), and Biochem. *Cell Biol.* 70: 365 (1992), reported similar findings, but instead used a histidine analog in place of a histidine-deficient medium. These findings led to the conclusion by Warrington (1986), supra, that cancer chemotherapeutic agents are selective when the tumor cell population has a higher growth fraction than normal cells. Thus, arresting the growth of normal cells without impacting the growth of tumor cells would confer selectivity to the anti-proliferative drugs commonly used in cancer chemotherapy.

In this context, a histidine ammonia lyase is a suitable candidate to selectively deplete the circulating histidine, since the histidine depleting activity of histidine ammonia lyase will cause growth arrest in normal cells, without affecting the growth of tumor cells. A histidine ammonia lyase can also be used in combination with a histidine analog such as L-histidinol, where the histidine ammonia lyase activity is not substantially decreased in the presence of the histidine analog. Accordingly, chemotherapeutic drugs would be less inclined to react with quiescent cells and confer less toxicity to a patient, thereby increasing the therapeutic index of cancer chemotherapy.

In one embodiment, patients who would undergo cancer chemotherapy first can be given an injection of an effective dose of a histidine ammonia lyase (e.g. between 1 μ g and 1 gram per kg body weight, administered intravenously). About twenty-four hours after histidine ammonia lyase injection, a conventional chemotherapeutic agent, such as one of those described herein, can then be administered to the patient. However, the invention also contemplates a method of administering several doses of a conventional chemotherapeutic agent to a patient after about 24 hours following the injection of a histidine ammonia lyase. The type of chemotherapy will vary with the type of cancer and also will be based on the suitability of the chemotherapeutic agent to a particular patient.

In yet another aspect of the invention, a histidine ammonia lyase can be used to enhance the specificity of cancer gene therapy. Retroviral vectors are one of the commonly used vehicles to deliver therapeutic genes for selectively killing tumor cells. However, retroviruses deliver DNA into growing cells without significant capacity to discriminate between cycling normal and cycling tumor tissues. Accordingly, retroviral therapy also suffers from the problem of killing high concentrations of non-targeted, healthy (i.e. non-tumor) cells that are proliferating at a given time in the human body. To obviate these problems, a histidine ammonia lyase can be first administered to a patient, thereby causing normal (i.e. non-tumor) cells to enter a reversible quiescent state. For example, an intravenous injection of 1 μ g to 1 g of HAL reacted with polyethylene glycol ("PEGylated HAL") per kg body weight can be given to a patient 24 hours prior to the injection of retroviral vector. This treatment would arrest the growth of normal cells without affecting the growth of cancer cells. As a result, retroviral vectors would selectively target proliferating tumor cells.

Immunosuppressant Properties

In another embodiment, the invention contemplates methodologies for delivering an immunosuppressant to a patient. The products of the enzymatic action of histidine ammonia lyase are trans-urocanic acid (t-UA) and ammonia. Irradiation at approximately 310 nm causes the photoisomerization of t-UA to its cis isomer (c-UA), as noted by Hanson et al., *Proc. Natl. Acad. Sci. U.S.A.* 95: 10576–10578 (1998). Cis-urocanic acid is believed to play the role of one of the UVB-induced immunosuppressive mediators (Kripke, *Cancer Res.* 54: 6102–6105 (1994); and Norval et al., *Photochem. Photobiol.* 62: 209–217 (1995)). This immunosuppressive property of urocanic acid can be used, for example, to treat immune system disorders and to prevent rejection of transplanted organs.

Although in theory, such an approach promises to provide a therapeutic benefit, small molecules like urocanic acid are rapidly cleared from circulation, thereby limiting their use as effective immunosuppressors over prolonged periods of time. However, it has been discovered that PEGylated HAL has a long circulatory half-life in mice (over 48 hours). Thus, an effective dose (1 μ g to 1 g per kg body weight) of a histidine ammonia lyase can be used to generate circulating urocanic acid for prolonged periods of time. In turn, a cis-isomerizing agent, such as UVB irradiation, can be used to cause local immunosuppression (for conditions such as psoriasis), or systemic immunosuppression, the process of which subjects the patient to whole body irradiation. In one example, whole body irradiation can be employed according to the invention, to combat organ rejection following transplantation.

In another embodiment, selective immunosuppression can be achieved by targeting the UVB irradiation. For example, psoriasis could be treated by an injection of a histidine ammonia lyase followed by selective irradiation of the affected areas. Selective UVB irradiation, following the injection of a histidine ammonia lyase into a patient, can also be used to treat conditions like arthritis.

In a further embodiment, localization and/or specificity of immunosuppression could also be achieved by targeting a histidine ammonia lyase to specific organs. To this end, the invention contemplates a fusion protein comprising one or more targeting peptide sequences in addition to the coding regions of a selected histidine ammonia lyase. Pasqualini et al. *Nature* 380: 364–366 (1996), have reported the success of targeting various proteins to specific organs via this methodology.

Treatment Methods

Therapeutic methods involve administering to a subject in need of treatment a therapeutically effective amount of a polypeptide contemplated by the invention. “Therapeutically effective” is employed here to denote the amount of a peptide that is of sufficient quantity to inhibit or reverse cancer growth (e.g., induce apoptosis). Some methods contemplate combination therapy with known cancer medications or therapies, for example, chemotherapy (preferably using compounds of the sort listed above) or radiation. The patient may be a human or non-human animal. A patient typically will be in need of treatment when suffering from a pathology such as a cancer or virus described above.

As previously demonstrated, the histidine ammonia lyase activity of the novel polypeptide is not substantially decreased in the presence of a histidine analog, like histidinol. A typical method, accordingly, involves administering to a patient both the novel polypeptide and the selected histidinol according to the methods described herein. In one embodiment, the novel polypeptide can be administered

simultaneously with a chosen histidinol. In another embodiment, the novel polypeptide is first administered to a patient, followed by a selected histidinol. In yet another embodiment, a histidine analog, such as histidinol, is first administered to a patient followed by the novel polypeptide. The invention also contemplates administering multiple dosages of the novel polypeptide or chosen histidinol in conjunction with the methods described herein (i.e. administering two or more dosages of the novel polypeptide, followed by at least one dosage of a histidine analog, like histidinol).

Administration during in vivo treatment may be by any number of routes, including parenteral and oral, but preferably parenteral. Intracapsular, intravenous, intrathecal, and intraperitoneal routes of administration may be employed, and generally intravenous is preferred. The skilled artisan will recognize that the route of administration will vary depending on the disorder to be treated.

Determining a therapeutically effective amount of the novel polypeptide, according to this invention, largely will depend on particular patient characteristics, route of administration, and the nature of the disorder being treated. General guidance can be found, for example, in the publications of the International Conference on Harmonisation and in REMINGTON’S PHARMACEUTICAL SCIENCES, chapters 27 and 28, pp. 484–528 (Mack Publishing Company 1990).

Determining a therapeutically effective amount specifically will depend on such factors as toxicity and efficacy of the medicament. Toxicity may be determined using methods well known in the art and found in the foregoing references. Efficacy may be determined utilizing the same guidance in conjunction with the methods described below in the Examples. A pharmaceutically effective amount, therefore, is an amount that is deemed by the clinician to be toxicologically tolerable, yet efficacious. Efficacy, for example, can be measured by the induction or substantial induction of T lymphocyte cytotoxicity at the targeted tissue or a decrease in mass of the targeted tissue.

Suitable dosages can be preferably from about one microgram per kg body weight to one gram per kg body weight, and more preferably from 2 milligrams to 10 mg per kg body weight.

The compositions, since they are useful in cancer treatment, may be formulated in conjunction with other conventional methods of treatment. Conventional methods include administering a histidine analog, like histidinol. Such forms of treatment also include conventional chemotherapeutic agents. Conventional chemotherapeutic agents include alkylating agents, antimetabolites, various natural products (e.g., vinca alkaloids, epipodophyllotoxins, antibiotics, and amino acid-depleting enzymes), hormones and hormone antagonists. Specific classes of agents include nitrogen mustards, alkyl sulfonates, nitrosoureas, triazines, folic acid analogues, pyrimidine analogues, purine analogs, platinum complexes, adrenocortical suppressants, adrenocorticosteroids, progestins, estrogens, antiestrogens and androgens. Some exemplary compounds include cyclophosphamide, chlorambucil, methotrexate, fluorouracil, cytarabine, thioguanine, vinblastine, vincristine, doxorubicin, daunorubicin, mitomycin, cisplatin, hydroxyurea, prednisone, hydroxyprogesterone caproate, medroxyprogesterone, megestrol acetate, diethyl stilbestrol, ethinyl estradiol, tomosifen, testosterone propionate and fluoxymesterone. In treating breast cancer, for example, tamoxifen is particularly preferred.

The invention further contemplates the administering to a patient a peptide of the invention in conjunction with

alkylating agents, antimetabolites, various natural products (e.g., vinca alkaloids, epipodophyllotoxins, antibiotics, or amino acid-depleting enzymes) hormones and hormone antagonists. Specific classes of agents include nitrogen mustards, alkyl sulfonates, nitrosoureas, triazenes, folic acid analogues, pyrimidine analogues, purine analogs, platinum complexes, adrenocortical suppressants, adrenocorticosteroids, progestins, estrogens, antiestrogens and androgens. Some exemplary compounds include cyclophosphamide, chlorambucil, methotrexate, fluorouracil, cytarabine, thioguanine, vinblastine, vincristine, doxorubicin, daunorubicin, mitomycin, cisplatin, hydroxyurea, prednisone, hydroxyprogesterone caproate, medroxyprogesterone, megestrol acetate, diethyl stilbestrol, ethinyl estradiol, tomosifen, testosterone propionate and fluoxymesterone.

Construction of the Inventive Polypeptide

A polypeptide according to this invention can be isolated by conventional means and the present invention is not limited to any particular method of producing the desired polypeptide contemplated herein. According to the contemplated recombinant methods of production, however, the invention provides recombinant DNA constructs comprising one or more of the nucleotide sequences of the domains described in the present invention. The recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a DNA or DNA fragment, typically bearing an open reading frame, is inserted, in either orientation. The invention further contemplates cells containing these vectors.

To this end, the DNA that encodes a novel polypeptide is first isolated using well known techniques. For instance, Example 1 provides one non-limiting method for isolating such targeted genomic DNA. This methodology includes culturing selected cells before extracting the genomic DNA from the culture, followed by subjecting the DNA to a series of restriction enzymes, whereby generated genomic DNA fragments can be studied and isolated by conventional techniques, for example, agarose gel electrophoresis.

Next, a vector can be selected and, likewise, cut with a restriction enzyme to generate a vector fragment by a methodology that is consistent with the procedure used to isolate the genomic DNA. Suitable vectors include bacterial and mammalian expression systems, as described below. After a suitable vector is selected, varying concentrations of the DNA fragment ("insert") can be placed into contact with the vector, as shown in Example 1, to determine the best insert:vector ratio for transformation of the DNA fragments. The transformants can then be cultured to generate copies of the DNA fragments.

To isolate the domains of a novel polypeptide from the generated DNA fragment, DNA probes can be designed by virtue of selecting sequences that are highly conserved in known histidine ammonia lyases. As shown in Example 1, the Wisconsin Graphics GCG package pileup program provides one method of determining highly conserved regions. A selected probe can be used to screen the targeted genomic DNA library, for example, using technology as disclosed by Ausubel et al., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, (John Wiley & Sons, 1994). Example 1 provides a non-limiting embodiment for utilizing suitable probes to screen the genomic library, followed by a series of steps to purify the genomic clones.

Bacterial Expression

Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and ter-

mination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and, if desirable, to provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may, also be employed as a matter of choice. In a preferred embodiment, the prokaryotic host is *E. coli*, as shown in Example 3.

Bacterial vectors may be, for example, bacteriophage-, plasmid- or cosmid-based. These vectors can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids typically containing elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, GEM 1 (Promega Biotec, Madison, Wis., USA), pBS, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pKK232-8, pDR540, and pRIT5 (Pharmacia). A preferred vector according to the invention is Bluescript vector (pBSSK)—(Stratagene).

These "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Bacterial promoters include lac, T3, T7, lambda P_R or P_L, trp, and ara. The T7 promoter is preferred.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is derepressed/induced by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Eukaryotic Expression

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include selected mouse L cells, such as thymidine kinase-negative (TK) and adenine phosphoribosyl transferase-negative (APRT) cells. Other examples include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking non-transcribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required non-transcribed genetic elements.

Mammalian promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Exemplary mammalian vectors include pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, and pSVL (Pharmacia).

In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, the coding sequence of interest may be ligated to an adenovirus transcription/translation control complex, e.g., the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus genome by in vitro or in vivo

recombination. Insertion in a non-essential region of the viral genome (e.g., region E1 or E3) will result in a recombinant virus that is viable and capable of expressing a target protein in infected hosts. (E.g., See Logan et al., 1984, *Proc. Natl. Acad. Sci. USA* 81:3655–3659).

Extension of Half-life and Prevention of Antibody Formation to the Inventive Peptide (PEGylating)

The invention also contemplates a polypeptide that can be induced to have an increased half-life. To this end, the polypeptide is manipulated by conventional techniques, such as modification with polyethylene glycol (PEGylation). According to this methodology, a suitable amount of a PEGylating agent is reacted with a polypeptide of the invention before introducing the polypeptide to a targeted cell culture or tissue. In one embodiment, the PEGylating agent is BTC-PEG 5000 (Shearwater Polymers, Inc.); however, the invention contemplates other PEGylating agents. Example 10 provides a non-limiting method to construct a PEGylated peptide in accordance with the invention.

A PEGylated polypeptide has practical applications both in vitro and in vivo. For example, a polypeptide's ability to sustain its enzymatic properties for an increased amount of time would permit a decrease in the dosage necessary to ameliorate one or more symptoms associated with a targeted pathology. In addition, a PEGylated polypeptide can possess an increased resistance to antibody-mediated depletion in the host. According to this embodiment, the PEGylating agent is believed to inhibit a host's antibody-mediated response against the polypeptide.

Gene Therapy Applications:

By virtue of discovering the DNA sequences that encode the novel polypeptides disclosed herein, the invention contemplates the use of these sequences in gene therapy approaches. To this end, a promoter and the DNA that encodes a polypeptide according to the invention is inserted into a vector, which is then introduced into a subject suffering from a pathology, such as a cancer or infectious virus.

The construction of a suitable vector can be achieved by any of the methods well-known in the art for the insertion of exogenous DNA into a vector. See, e.g., Sambrook et al., *Molecular Cloning* (Cold Spring Harbor Press 2d ed. 1989), which is incorporated herein by reference. In addition, the prior art teaches various methods of introducing exogenous genes into cells in vivo. See Rosenberg et al., *Science* 242:1575–1578 (1988), and Wolff et al., *PNAS* 86:9011–9014 (1989), which are incorporated herein by reference. The routes of delivery include systemic administration and administration in situ. Well-known techniques include systemic administration with cationic liposomes, and administration in situ with viral vectors. Any one of the gene delivery methodologies described in the prior art is suitable for the introduction of a recombinant vector containing an inventive gene according to the invention into a MTX-resistant, transport-deficient cancer cell. A listing of present-day vectors suitable for the purpose of this invention is set forth in Hodgson, *Bio/Technology* 13: 222 (1995), which is incorporated by reference.

For example, liposome-mediated gene transfer is a suitable method for the introduction of a recombinant vector containing an inventive gene according to the invention into a MTX-resistant, transport-deficient cancer cell. The use of a cationic liposome, such as DC-Chol/DOPE liposome, has been widely documented as an appropriate vehicle to deliver DNA to a wide range of tissues through intravenous injection of DNA/cationic liposome complexes. See Caplen et

al., *Nature Med.* 1:39–46 (1995) and Zhu et al., *Science* 261:209–211 (1993), which are herein incorporated by reference. Liposomes transfer genes to the target cells by fusing with the plasma membrane. The entry process is relatively efficient, but once inside the cell, the liposome-DNA complex has no inherent mechanism to deliver the DNA to the nucleus. As such, the most of the lipid and DNA gets shunted to cytoplasmic waste systems and destroyed. The obvious advantage of liposomes as a gene therapy vector is that liposomes contain no proteins, which thus minimizes the potential of host immune responses.

As another example, viral vector-mediated gene transfer is also a suitable method for the introduction of the vector into a target cell. Appropriate viral vectors include adenovirus vectors and adeno-associated virus vectors, retrovirus vectors and herpesvirus vectors.

Adenoviruses are linear, double stranded DNA viruses complexed with core proteins and surrounded by capsid proteins. The common serotypes 2 and 5, which are not associated with any human malignancies, are typically the base vectors. By deleting parts of the virus genome and inserting the desired gene under the control of a constitutive viral promoter, the virus becomes a replication deficient vector capable of transferring the exogenous DNA to differentiated, non-proliferating cells. To enter cells, the adenovirus fibre interacts with specific receptors on the cell surface, and the adenovirus surface proteins interact with the cell surface integrins. The virus penton-cell integrin interaction provides the signal that brings the exogenous gene-containing virus into a cytoplasmic endosome. The adenovirus breaks out of the endosome and moves to the nucleus, the viral capsid falls apart, and the exogenous DNA enters the cell nucleus where it functions, in an epichromosomal fashion, to express the exogenous gene. Detailed discussions of the use of adenoviral vectors for gene therapy can be found in Berkner, *Biotechniques* 6:616–629 (1988) and Trapnell, *Advanced Drug Delivery Rev.* 12:185–199 (1993), which are herein incorporated by reference. Adenovirus-derived vectors, particularly non-replicative adenovirus vectors, are characterized by their ability to accommodate exogenous DNA of 7.5 kB, relative stability, wide host range, low pathogenicity in man, and high titers (10^4 to 10^5 plaque forming units per cell). See Stratford-Perricaudet et al., *PNAS* 89:2581 (1992).

Adeno-associated virus (AAV) vectors also can be used for the present invention. AAV is a linear single-stranded DNA parvovirus that is endogenous to many mammalian species. AAV has a broad host range despite the limitation that AAV is a defective parvovirus which is dependent totally on either adenovirus or herpesvirus for its reproduction in vivo. The use of AAV as a vector for the introduction into target cells of exogenous DNA is well-known in the art. See, e.g., Lebkowski et al., *Mole. & Cell. Biol.* 8:3988 (1988), which is incorporated herein by reference. In these vectors, the capsid gene of AAV is replaced by a desired DNA fragment, and transcomplementation of the deleted capsid function is used to create a recombinant virus stock. Upon infection the recombinant virus uncoats in the nucleus and integrates into the host genome.

Another suitable virus-based gene delivery mechanism is retroviral vector-mediated gene transfer. In general, retroviral vectors are well-known in the art. See Breakfield et al., *Mole. Neuro. Biol.* 1:339 (1987) and Shih et al., in *Vaccines* 85: 177 (Cold Spring Harbor Press 1985). A variety of retroviral vectors and retroviral vector-producing cell lines can be used for the present invention. Appropriate retroviral vectors include Moloney Murine Leukemia Virus, spleen

necrosis virus, and vectors derived from retroviruses such as Rous Sarcoma Virus, Harvey Sarcoma Virus, avian leukosis virus, human immunodeficiency virus, myeloproliferative sarcoma virus, and mammary tumor virus. These vectors include replication-competent and replication-defective retroviral vectors. In addition, amphotropic and xenotropic retroviral vectors can be used. In carrying out the invention, retroviral vectors can be introduced to a tumor directly or in the form of free retroviral vector producing-cell lines. Suitable producer cells include fibroblasts, neurons, glial cells, keratinocytes, hepatocytes, connective tissue cells, ependymal cells, chromaffin cells. See Wolff et al., *PNAS* 84:3344 (1989).

Retroviral vectors generally are constructed such that the majority of its structural genes are deleted or replaced by exogenous DNA of interest, and such that the likelihood is reduced that viral proteins will be expressed. See Bender et al., *J. Virol.* 61:1639 (1987) and Armento et al., *J. Virol.* 61:1647 (1987), which are herein incorporated by reference. To facilitate expression of the novel protein, a retroviral vector employed in the present invention must integrate into the genome of the host cell genome, an event which occurs only in mitotically active cells. The necessity for host cell replication effectively limits retroviral gene expression to tumor cells, which are highly replicative, and to a few normal tissues. The normal tissue cells theoretically most likely to be transduced by a retroviral vector, therefore, are the endothelial cells that line the blood vessels that supply blood to the tumor. In addition, it is also possible that a retroviral vector would integrate into white blood cells both in the tumor or in the blood circulating through the tumor.

The spread of retroviral vector to normal tissues, however, is limited. The local administration to a tumor of a retroviral vector or retroviral vector producing cells will restrict vector propagation to the local region of the tumor, minimizing transduction, integration, expression and subsequent cytotoxic effect on surrounding cells that are mitotically active.

Both replicatively deficient and replicatively competent retroviral vectors can be used in the invention, subject to their respective advantages and disadvantages. For instance, for tumors that have spread regionally, such as lung cancers, the direct injection of cell lines that produce replication-deficient vectors may not deliver the vector to a large enough area to completely eradicate the tumor, since the vector will be released only from the original producer cells and their progeny, and diffusion is limited. Similar constraints apply to the application of replication deficient vectors to tumors that grow slowly, such as human breast cancers which typically have doubling times of 30 days versus the 24 hours common among human gliomas. The much shortened survival-time of the producer cells, probably no more than 7-14 days in the absence of immunosuppression, limits to only a portion of their replicative cycle the exposure of the tumor cells to the retroviral vector.

The use of replication-defective retroviruses for treating tumors requires producer cells and is limited because each replication-defective retrovirus particle can enter only a single cell and cannot productively infect others thereafter. Because these replication-defective retroviruses cannot spread to other tumor cells, they would be unable to completely penetrate a deep, multilayered tumor in vivo. See Markert et al., *Neurosurg.* 77: 590 (1992). The injection of replication-competent retroviral vector particles or a cell line that produces a replication-competent retroviral vector virus may prove to be a more effective therapeutic because a replication competent retroviral vector will establish a productive infection that will transduce cells as long as it

persists. Moreover, replicatively competent retroviral vectors may follow the tumor as it metastasizes, carried along and propagated by transduced tumor cells. The risks for complications are greater, with replicatively competent vectors, however. Such vectors may pose a greater risk than replicatively deficient vectors of transducing normal tissues, for instance. The risks of undesired vector propagation for each type of cancer and affected body area can be weighed against the advantages in the situation of replicatively competent versus replicatively deficient retroviral vector to determine an optimum treatment.

Both amphotropic and xenotropic retroviral vectors may be used in the invention. Amphotropic viruses have a very broad host range that includes most or all mammalian cells, as is well known to the art. Xenotropic viruses can infect all mammalian cells except mouse cells. Thus, amphotropic and xenotropic retroviruses from many species, including cows, sheep, pigs, dogs, cats, rats, and mice, inter alia can be used to provide retroviral vectors in accordance with the invention, provided the vectors can transfer genes into proliferating human cells in vivo.

Clinical trials employing retroviral vector therapy treatment of cancer have been approved in the United States. See Culver, *Clin. Chem.* 40: 510 (1994). Retroviral vector-containing cells have been implanted into brain tumors growing in human patients. See Oldfield et al., *Hum. Gene Ther.* 4: 39 (1993). These retroviral vectors carried the HSV-1 thymidine kinase (HSV-tk) gene into the surrounding brain tumor cells, which conferred sensitivity of the tumor cells to the antiviral drug ganciclovir. Some of the limitations of current retroviral based cancer therapy, as described by Oldfield are: (1) the low titer of virus produced, (2) virus spread is limited to the region surrounding the producer cell implant, (3) possible immune response to the producer cell line, (4) possible insertional mutagenesis and transformation of retroviral infected cells, (5) only a single treatment regimen of pro-drug, ganciclovir, is possible because the "suicide" product kills retrovirally infected cells and producer cells and (6) the bystander effect is limited to cells in direct contact with retrovirally transformed cells. See Bi et al., *Human Gene Therapy* 4: 725 (1993).

Yet another suitable virus-based gene delivery mechanism is herpesvirus vector-mediated gene transfer. While much less is known about the use of herpesvirus vectors, replication-competent HSV-1 viral vectors have been described in the context of antitumor therapy. See Martuza et al., *Science* 252: 854 (1991), which is incorporated herein by reference.

The following examples are intended to be illustrative and not limiting.

WORKING EXAMPLES

Example 1

Isolation of the DNA Encoding HAL

The bacterium from the family Corynebacteriaceae that produces bioactive histidine ammonia lyase (HAL) was grown in 100 ml of Luria broth overnight at 30° C. The cells were harvested and resuspended in 10 ml of 50 mM Tris (pH 7.5) with 10 mM EDTA. Solid lysozyme was added to 0.2 mg/ml and the suspension was incubated at 4° C. for 30 minutes. Following this incubation, the suspension was frozen for several hours at -70° C. Upon thawing, SDS was added to 0.1% and proteinase K was added to 0.2 mg/ml and was incubated at 37° C. overnight. Next, RNase was added to 0.1 mg/ml and the mixture incubated at 55° C. for 30

minutes. The resulting DNA was extracted five times with an equal volume of phenol/chloroform (1:1) and precipitated with 2 volumes of absolute ethanol. The DNA was spooled out on a glass Pasteur pipette, washed with ice cold 70% ethanol, and resuspended in a minimal amount of TE buffer.

Genomic DNA was restricted with Sau3AI over a time course of 1 hour. Every ten minutes, an aliquot was removed, taken to 10 mM EDTA, and analyzed by agarose gel electrophoresis. The time point that showed an average fragment size of 1–5 kb was loaded in its entirety and resolved on an agarose gel. The 1–5 kb fragments were isolated with DEAE filter paper, phenol extracted and ethanol precipitated.

The Bluescript vector pBSSK—(Stratagene) was restricted with BamHI and treated with arctic shrimp alkaline phosphatase (USB). The treated, linearized vector was subjected to agarose gel electrophoresis and the linear species were isolated as above with DEAE filter paper.

The resulting vector and genomic DNA fragment concentrations were measured and ligations conducted. These were done using 150 ng of vector in a 10 μ l reaction volume. Vector concentration was kept constant and insert was varied at stoichiometries of 0 \times , 0.5 \times , 1 \times , 2 \times , and 5 \times that of the vector. Ligations were performed at 4 $^{\circ}$ C. overnight. After ligation, reactions were diluted to 30 μ l with water and heated to 65 $^{\circ}$ C. for ten minutes.

The diluted ligation reactions were used to transform freshly prepared electrocompetent XL-1Blue MRF' (Stratagene) cells. Transformed ligations were test plated on MacConkey agar to judge the best insert:vector ratio. Once the optimum ratio had been determined, this was used exclusively for transformation.

Transformants were plated at a cell density of 3 000–10 000 cfu per nylon filter on 150 mm plates containing LB agar with 50 μ g/ml ampicillin. Duplicate replica filters were produced and processed for colony hybridization.

DNA probes were designed using regions of known histidine ammonia lyases that had a strong probability of being conserved in HAL. Using the Wisconsin Graphics GCG package pileup program, the peptide sequences of the known histidine ammonia lyases from *B. subtilis*, *S. griseus*, *P. putida*, and rat were aligned and examined for highly conserved regions. Several of these were chosen as candidates for probe design. Using the DNA sequences of cloned genes from *Corynebacterium*, a codon preference table was derived. From this a backtranslation was performed resulting in the most likely DNA sequence for the protein region of interest.

Two of the resulting probes (TM63 and TM74), shown in Table 1, below, were labeled, mixed, and used to screen the above genomic library. Oligos were labeled with γ^{32} PATP using T4 polynucleotide kinase as described (Ausubel, et al, eds, 1994. "Current Protocols in Molecular Biology," John Wiley and Sons, Inc.) and cleaned up using Elutipis (Schleicher & Schuell). Hybridization of duplicate filters was carried out in a Bellco hybridization oven at 37 $^{\circ}$ C. using the SSPE protocol as described (Ausubel, et al., eds, "Current Protocols in Molecular Biology," John Wiley and Sons, Inc., 1994). Filters were washed in 6 \times SSC with 0.5% SDS (Ausubel, et al, eds, "Current Protocols in Molecular Biology," John Wiley and Sons, Inc., 1994) at 37 $^{\circ}$ C. Filters were then washed at successively higher temperatures in 3 M TMAC (Ausubel, et al, eds, "Current Protocols in Molecular Biology," John Wiley and Sons, Inc., 1994) until very little radioactivity could be detected with a survey meter (generally 45–55 $^{\circ}$ C.). Upon exposure to X-Ray film (Kodak X-Omat), colonies which were evident on both replicate filters were picked with a wooden toothpick and transferred to a fresh nylon filter overlaid onto an LB/ampicillin plate. This procedure was repeated until a homogeneous population was achieved.

TABLE 1

Name	Length	Sequence (5' to 3')	Coordinates
TM63	30	CGCGTTCAGGACGCATACTCCGTTTCGCTGC	838–867
TM74	24	GCCCATGGAACGTGGTCTTCCTG	1370–1393
TM85	21	ATCATCATGCCCCGAGTCCACA	1156–1176
TM87	21	GCCATCAGGAAGACCACGTTT	990–971
TM89	20	ATGCAGGAAGACCACGTTTC	1246–1265
TM91	21	ATCGAGGTCCGCCAATGCCAT	648–628
TM92	18	ACCGGAGCAGCCCAGTGA	441–424
TM93	20	TGCTTGAAGTATTGCGCCAG	1403–1422
TM94	18	GATCCTCGGGTGCGATGT	226–209
TM95	18	ATGCTGATCGGGCTTCGT	92–74
TM96	27	ATTTGATTCAATATGGCTTCCGCTCCTC	–11–+16
TM97	28	ATCTTGGATCCGAACATGGTGCCTTGCA	Beyond C-Terminus
TM98	18	AGCACCAGAT CGATGCAC	128–145

TABLE 1—continued

Name	Length	Sequence (5' to 3')	Coordinates
TM99	18	TGGCATGGGTGAACCGGT	267–284
TM101	18	ATCAGCGTTGAAGCCCAG	682–699
TM103	18	ACGTGCTGGACTTCCTTG	1019–1036
TM105	18	GTGCATAAGGCCCTCGAA	1501–1518
TM106	18	GAGCTTCGAGGGCCTTAT	1522–1505
TM109	18	CGAGCAACGCAGCGAGTA	870–853

Purified clones were confirmed by DNA sequencing and comparison to known peptide sequence and to known histidine ammonia lyases from the literature as well as peptide sequence from authentic histidine ammonia lyase from a bacterium belonging to the family Corynebacteriaceae. Using this protocol a primary clone, pHUT23, was isolated and identified as containing HAL coding sequence.

An oligo, TM85, was synthesized to the N-terminal-most region of pHUT23 and used to further screen the genomic library. This resulted in two clones, pHUT26 and pHUT28 which contain sequences more toward the N-terminus of the gene. These clones represent the C-terminal $\frac{2}{3}$ of the gene. Another oligo, TM91, was synthesized based on the N-terminal-most sequence. This oligo was used to re-screen existing library plates. This resulted in the isolation of pHUT30, containing the N-terminal $\frac{1}{3}$ of the gene. The authenticity of this gene was confirmed by comparison of peptide sequences obtained from the original enzyme isolated from a bacterium from the family Corynebacteriaceae.

Using both the full-length gene and the genomic sub-clones, the histidine ammonia lyase gene was sequenced in both directions by Sanger's chain-termination DNA sequencing method (USB). The purified double-stranded templates, shown with the primers used in Table 1, were denatured by the standard alkaline-denaturation method.

The sequence data revealed that the intact gene encompasses 1533 base pairs (see SEQ ID NO: 12), encoding a protein of 511 amino acids (see SEQ ID NO: 10). Expression of this open reading frame in *E. coli* results in a single, approximately 55 kDa polypeptide, as detected by denaturing polyacrylamide gel electrophoresis (see FIG. 5). Appearance of this 55 kDa peptide corresponds with induction of histidine ammonia lyase activity (conversion of L-histidine to urocanic acid), an activity detected by us under these conditions exclusively in *E. coli* harboring a plasmid containing the full-length HAL gene.

Example 2

Peptide Sequencing of HAL

HAL from a bacterium from the family Corynebacteriaceae that had been partially purified using ammonium sulfate and DEAE—Sephadex was resolved by SDS-PAGE. The separated material was electrophoretically transferred to Immobilon-P and stained with Coomassie Brilliant Blue. The major band of 55 000 daltons was excised and subjected to N-terminal sequencing. This fraction was sent to Commonwealth Biotechnologies, Inc. (Richmond, Va.), cleaved with BrCN, HPLC purified, and fractions sequenced.

Example 3

Expression of Histidine Ammonia Lyase from a Bacterium from the Family Corynebacteriaceae Using a High-Efficiency Prokaryotic Expression System

The *E. coli* expression plasmid pHUT102, depicted in FIG. 4, is designed to express HAL DNA sequences from the strong phage T7 gene 10 promoter using T7 RNA Polymerase. This vector, pSN75, is a derivative of pET11b (Novagen) that has an additional transcriptional terminator inserted upstream of the T7 promoter. This provides the target cassette in as transcriptionally silent a context as possible.

Two mutagenic oligonucleotides, TM96 and TM97 (see Table 1), were synthesized based on histidine ammonia lyase sequence. The N-terminal oligo adds an NdeI site at the ATG start codon and the C-terminal oligo adds a BamHI site just beyond the C-terminus. These were used to thermal cycle amplify the HAL gene out of the genome of a bacterium from the family Corynebacteriaceae. The resulting fragment was restricted with NdeI and BamHI and cloned into pSN75, resulting in pHUT102. This provides histidine ammonia lyase under the control of a T7 promoter with flanking transcriptional terminators to prevent readthrough transcription.

A T7 expression system containing kanamycin as a selectable marker was constructed by cloning the 1 kb kanamycin resistance Pst I cassette excised from pUC4K into the unique Pst I site of pSN75. The new vector, pSN75K is ampicillin sensitive and kanamycin resistant. The Nde I–BamHI fragment containing the HAL coding region was excised from pHUT102 and cloned into NdeI+BamHI cut pSN75K. This expression construct, pHUT200, could readily be used for clinical production of HAL since there is no need to use penicillin antibiotics during the production.

For the purpose of expression, pHUT200 was transformed into BL21(λ DE3) harboring pLysS and grown in Terrific broth at 28° C. to OD600 of 0.6. The culture was induced for 4 hours with 0.4 mM IPTG and harvested. Cells were lysed and analyzed by SDS-PAGE and enzyme assay. As measured by these assays, we estimate that the HAL is produced to approximately 30% of the total cell protein (see FIG. 5) and 8% of the soluble protein, representing about 0.2 g per liter of culture.

Example 4

Expression of HAL in a Vector that Directs Periplasmic Localization

The NdeI/BamHI fragment from pHUT102 was excised and purified. The vector, pET12c (Novagen), was likewise

cut with NdeI/BamHI and purified. These fragments were ligated and transformed into XL-1 Blue MRF'. The clone, pHUT114, containing the HAL gene as a fusion with a T7 phage periplasmic localization signal under control of a T7 promoter.

For the purpose of expression, pHUT114 was transformed into BL21(λ DE3) and grown in Terrific broth supplemented with 75 mM NaCl at 28° C. to OD₆₀₀ of 0.6 under antibiotic selection. The culture was induced for 4 hours with 0.4 mM IPTG and harvested. Spheroplasts were prepared (Ausubel, et al, eds, "Current Protocols in Molecular Biology," John Wiley and Sons, Inc., 1994) and the supernatant was assayed for enzyme.

This approach yielded active, periplasmic HAL. However, microscopic examination showed the formation of inclusion bodies. This resulted in relatively low per volume yield and a specific activity comparable to the cellularly localized material. At this point, this approach offers no clear advantage. However, if inclusion body formation could be minimized by altering growth and induction conditions, it is possible that the enzyme could be purified directly from the culture medium.

Example 5

Fed Batch Fermentation for the Production of HAL from a Bacterium from the Family Corynebacteriaceae

Fermentation of pHUT200 in BL21 λ 21(DE3)pLysS is performed at 30° C. in the following media: Base media—20 g/L yeast extract and 1.67 g/L (NH₄)₂SO₄, supplemented with 17.2 ml of 1 M KH₂PO₄, 36.7 ml of 1 M K₂HPO₄, 1 ml/L of 2% CaCl₂·H₂O, 1 ml/L of 10% thiamine-HCl, 10 ml/L of Trace Metal Solution (6 g/liter Fe(III)Citrate, 1.5 g/L MnCl₂·H₂O, 0.8 g/L Zn(CH₃COO)₂·2H₂O, 0.3 g/L H₃BO₃, 0.25 g/L Na₂MoO₄·2H₂O, 0.25 g/L CoCl₂·6H₂O, 0.15 g/L CuCl₂·2H₂O, 0.84 g/L EDTA), 10 ml/L of 20% MgSO₄·7H₂O, and 10 ml/L of 50% glucose. Bring to final volume of 1 Liter with ddH₂O. When pH increases by 0.01 the feed media is initiated. The feed media is as follows: 1.5 g/L (NH₄)₂SO₄, 274 g/L yeast extract, 7.5 ml/L MgSO₄·7H₂O, and 400 ml 50% glucose. The feed was stopped when the pH decreased by 0.01. Thus, pH was maintained by the feed control loop. The fermentation run is induced at OD₆₀₀=5.0 with 1 mM IPTG. The dissolved oxygen is maintained at 20%, and induction is continued for 4 hours. The final OD₆₀₀=32, and the yield is approximately 1 gram of HAL per liter. The amount of protein following different periods of induction is shown in the SDS-PAGE gel in FIG. 5.

Example 6

Purification of HAL from *E. coli*

A simple purification method involving two acetone precipitation steps and one Q-sepharose column. Following resuspension of the cell paste in one-tenth volume of 50 mM TRIS pH 8.0 the pellet is sonicated four times and centrifuged. An equal volume of acetone is added to the supernatant. The solution is then centrifuged at 14,000 rpm for 15 minutes. The supernatant is retained and an equal volume of acetone is again added and again centrifuged. Following the second acetone precipitation the pellet is resuspended in 50 mM TRIS pH 8.0. The resuspension is then loaded onto a Q-sepharose column (5 mg protein/ml Q-sepharose) in 20 mM TRIS pH 8.0. The column is then washed with 20 mM

TRIS pH 8.0 with 0.1 M KCl. Elution is performed with a 200 ml gradient from 0.1 M to 0.6 M KCl at a flow rate of 1 ml/min. Phenyl sepharose can then be used to further purify the enzyme. An example of purification via this scheme is depicted in FIG. 6.

Several potential alternate methods of purification have also been used successfully. HAL is resistant to heating at 70° C. Thus, heating and centrifugation can be used to remove precipitated contaminant proteins. Additionally, HAL does not precipitate with the addition of ammonium sulfate to 30% saturation. Therefore, addition of 30% ammonium sulfate and centrifugation can also be used to remove contaminant proteins. This precipitation can then be followed by purification via a phenyl sepharose column.

Example 7

Recovery of HAL from Inclusion Bodies

The pellet obtained from the sonicate of EXAMPLE 6 was washed in 100 mM sodium phosphate, pH6 containing 0.5% Triton X-100 by trituration. The washed inclusion bodies were collected by centrifugation at 4° C. in an SS34 rotor at 10 000 rpm for 10 minutes. This was repeated twice more, resulting in purified inclusion bodies.

A small amount of this material was solubilized in 50 mM Tris, pH8 with 8 M urea. Two hundred micrograms of this material was bound to 0.5 ml of DEAE—sephadex equilibrated in the same buffer. The resin was collected by centrifugation and eluted with 1 ml of 50 mM Tris, pH8 with 0.5 M NaCl. This material was directly assayed for histidine ammonia lyase activity. A typical recovery yielded approximately 1–5% of the total histidine ammonia lyase in the active conformation.

Example 8

Characterization of HAL

Purified HAL has been determined to have approximately 40 I.U./mg of activity at 37° C. The temperature optimum was found to be 45° C. (FIG. 7). The graph shows that the enzyme maintains a significant level of activity at physiological temperature conditions. The activity profile of HAL at various pH is depicted in FIG. 8. The enzyme is active over a wide range of pH, with highest activity around pH 8.2 and high activity in physiological conditions.

Both reduced glutathione and DTT caused inhibition of HAL, but the inhibition was not complete. Both compounds were required at 15 mM concentrations to reduce the activity by half. EDTA was found to completely inhibit the reaction in concentrations as low as 1 mM. This inhibition was reversible with the presence of Mn²⁺ at 1×10⁵ M concentration.

Histidine ammonia lyase produced in *E. coli* was purified to near homogeneity as detailed above. Female mice weighing 18–22 grams were injected intraperitoneally with 1500 IU/kg body weight. HAL activity was monitored by assaying plasma obtained via retro-orbital bleeding two and ten hours following injection. These experiments using the recombinant enzyme showed an in vivo half-life of approximately 3 hours.

Example 9

Comparison of HAL to Other Histidine Ammonia Lyases

HAL has a significant advantage over other histidine ammonia lyases in that it is relatively resistant to inhibition

by L-histidinol. L-histidinol is a histidine analog. Because L-histidinol acts as a competitive inhibitor it must be present in high concentrations to have an effect on histidine dependent reactions. Using HAL to reduce the overall histidine pool would therefore greatly increase the effectiveness of L-histidinol. However, brother histidine ammonia lyase enzymes have been shown to be strongly inhibited by L-histidinol. Because the Corynebacteriaceae histidine ammonia lyase (HAL) is not inhibited by L-histidinol at therapeutic L-histidinol levels it has a great advantage over other histidine ammonia lyases. Histidine ammonia lyase isolated from *Achromobacter liquidum* and *Streptomyces griseus* have been shown to be inhibited by L-histidinol and L-histidinol phosphate respectively with a K_i of 4.58 and 0.27 mM (Shibatani, T. et al. 1975; Wu, P. C. et al. 1995). Enzyme kinetic studies in our laboratory using *Streptomyces griseus* histidine ammonia lyase, showed that L-histidinol was able to completely inhibit the enzyme even at equal molar concentration to histidine. However, with HAL 20% of activity still is retained when L-histidinol is present at 10 times the concentration of L-histidine. We demonstrated the K_i of L-histidinol for HAL to be 24.3 to 33.4 mM.

Example 10

Extension of Half-life and Prevention of Antibody Formation to HAL Using PEGylation

A PEGylation strategy has been developed using BTC-PEG 5000 (Shearwater Polymers, Inc.). HAL is reconstituted in 50 mM sodium phosphate buffer pH 8.0 and dialyzed against that same buffer. Dialysis is continued for three hours. Following dialysis the protein concentration is adjusted to 5 mg/ml. BTC-PEG is added in a ratio of 1:10 and incubated for one hour at RT after dissolving the BTC-PEG. The solution is then dialyzed against 50 mM sodium phosphate pH 7.5 to remove unbound PEG. The extent of PEGylation is then determined by using a fluorescamine assay. Different ratios of PEG to enzyme were tested to determine the % PEGylation each ratio would yield. Repeated fluorescamine assays showed that 1:10 PEGylation with BTC-PEG provided about 40–45% PEGylation protection of the enzyme.

When HAL was injected into mice, the bioactive half-life was determined to be less than four hours. To determine the half-life of the enzyme a known amount of units of enzyme is injected intraperitoneally into several mice. Blood is then drawn retro-orbitally from different mice at 4-hour intervals. The blood is then centrifuged and serum is used to perform the histidine ammonia lyase assay as previously described. The half-life is then determined by comparing the time at which units/ml in serum is half of its value following the first four hour time-point.

A 30 Unit HAL intraperitoneal injection yielded only 3 Units of active HAL in the blood following four hours and the half-life was found to be less than one hour. HAL was then PEGylated using BTC-PEG. This increased the half-life of the enzyme in the blood to more than 48 hours. The PEGylation of the enzyme also affords it protection against antibody-mediated depletion in the host. UnPEGylated protein will elicit an antibody response that will clear the enzyme from the blood following one week of treatment. The antibody response is greatly delayed in mice receiving PEGylated HAL. In three out of five mice active enzyme was still being recovered following 79 days of treatment and following 119 days in 2 of the five mice.

We have also used a higher molecular weight PEG, BTC 20,000, as well as other PEGs to successfully modify HAL.

Example 11

Anti-viral Activity of HAL

HAL was tested for its anti-viral activity against a variety of infectious viruses in vitro. Effectiveness against Herpes Simplex Virus (HSV) was assayed using the following method. Confluent VERO cells from a T-175 flask are trypsinized and split into as many T-25 flasks as the experiment requires. The cells are grown in RPMI-1640 with 10% newborn calf serum-heat inactivated, and L-glutamine. After cells have grown to confluence remove the media and add 0.5 ml of diluted virus (make a series of 1:5 dilution). Dilution of virus is prepared in RPMI-1640 with 2% NCS. The cells are then incubated for 1 hour at 37° C. and then 5 ml of RPMI-1640 with 2% NCS with or without the test compounds is added and incubation is allowed to continue for 1 day. After 24 hours the flasks are sealed with parafilm and frozen at -70° C. The cells are then allowed to thaw at RT to lyse dead intact cells, releasing virus. The viral suspension is then centrifuged to remove cell debris. The viral dilution that caused complete lysis will be used in the plaque assay. The plaque assay is set up by trypsinizing cells from a T-75 and resuspending the cells in RPMI-1640 with 10% NCS and poured into 6-well plate at 2 ml/well. The cells are incubated overnight at 37° C. The media is then removed by suction and 0.2 ml of the viral dilution is added and allowed to incubate for one hour. During this hour the agar is prepared and stored at 41° C. to prevent hardening. The agar concentrations are as follows: ½ vol. 2×BME (Gibco), 2% Pen/Strep, 2% NCS, and 1% agar. After the hour incubation 2 ml of the BME/agar is carefully added to the wells, so as not to disturb the cell monolayer. The plate is left at RT for twenty to thirty minutes to allow the agar to harden, and then the cells are incubated for 48 hours at 37° C. The cells are then stained used BME/agar containing neutral red. The BME/agar is prepared as before with the addition of neutral red stain (Gibco) to a final concentration of 5%. 2 ml of this agar is added and allowed to harden before 24 hour incubation at 37° C. Plaques are then counted and the cells fixed for a permanent record.

One positive experimental result has been seen against HSV. Herpes Simplex Viruses are double-stranded DNA viruses belonging to the family Herpesviridae. Several viruses in this group, including Herpes Simplex Virus Type 1, Herpes Simplex Virus Type 2, Varicella-Zoster Virus, Epstein-Barr Virus, and Cytomegalo Virus cause serious and often fatal infections in human beings. Results of the experiments using HSV have indicated that HAL does inhibit HSV replication and that when given in conjunction with L-histidinol even significantly greater inhibition is observed. Use of HAL alone in a concentration of 0.005 U/ml resulted in a reduction in plaque forming units of approximately 200 fold versus control. Use of 0.01 U/ml HAL resulted in over 1,000-fold decrease in plaque forming units/ml. However, when given in conjunction with L-histidinol the effect is greatly enhanced and the concentration of both compounds can be significantly lowered while inhibition is increased. When L-histidinol is given at 0.1 and 0.5 mM concentrations no inhibition is observed, and only 5-fold inhibition is observed at 1 mM. However, when 0.5 mM L-histidinol is given in combination with 0.003 U/ml HAL the inhibition is near 100% (less than 500 PFU versus 1.25×10^8 in control). These results are shown in FIG. 9.

Another successful study has been with Respiratory Syncytial Virus (RSV). RSV is another highly infectious disease causing agent. It causes lower respiratory-tract infections such as bronchitis and pneumonia in infancy and early

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childhood, with nearly 50% of infants suffering from an RSV infection during their first winter. Experiments were performed in tissue culture using the RSV Plaque Assay. The RSV plaque assay is performed similarly to the HSV assay. When performing the RSV assay Hep2 cells are used to propagate the RSV and the cells are grown in EMEM media with 2% FBS, L-glutamine and Antibiotic-Antimycotic. The virus stock is diluted in the medium and added to each well with or without the desired testing compound. The plates are incubated for 2 hours at 37° C. and the virus is removed. 0.5% agarose is added to the media and incubated for 5 days at 37° C. The plates are then fixed with 10% formalin and stained with crystal violet. When HAL and L-histidinol were present in 0.005 U/ml and 3 mM respectively, no inhibition of RSV plaque numbers is seen, as is shown in FIG. 11. However, when these same concentrations were used in combination the resulting plaque assay showed no higher than background levels of plaques. These results indicate the strong synergy that exists with these two drugs and provides promise for HAL as an effective antiviral therapy.

Use of HAL in combination with L-histidinol is thus shown to greatly reduce the therapeutic index of both drugs. This makes effective treatment of these highly infectious diseases with low toxicity a good possibility.

Rauscher Murine Leukemia Virus (RMuLV) belongs to the family retroviradae, the group of viruses that also includes the Human Immunodeficiency Virus (HIV). We have used RMuLV as a model for drug development against HIV. In these studies we use mouse SC-1 cells persistently infected with RMuLV to test the effect of HAL against virus replication. Briefly, the cells are plated on a 96-well plate in RPMI medium containing 10% Fetal Calf Serum and glutamine. After 24 hours of growth, the cells are treated with various test compounds for 24 hours. The supernatant is then tested for reverse transcriptase activity as described

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in Roberts, J. and W. G. McGregor (Roberts, J. and W. G. McGregor. 1991. *J. General Virology*. 72: 299-305). Results depicted in FIG. 12 show that HAL given at 0.004 U/ml inhibits reverse transcription by over 70%.

Example 12

Effectiveness of HAL as an Anticancer Agent

We have used a sensitive in vitro cancer drug screening assay to study the effect of HAL on various tumor cell lines. Briefly, each cell line is inoculated into microtiter plates, and pre-incubated for 24 hours at 37° C. Subsequently, the test agents are added and the culture is incubated for an additional 48 hours at 37° C. End-point determination of cell growth is performed by in situ fixation of cells, followed by staining with a protein-binding dye, sulforchodamine B (SRB) (Monks, A., Scudiero, D. Skehan, P., Shoemaker, R., Paull, L., Vistica, D., Hose, C., Langley, J., Cronise, P., Vaigro-Wolff, A. et al. 1991. *Journal of National Cancer Institute*. 83(11): 757-766). Two human prostate cancer cell lines, LNCaP and PC-3, were tested using this assay. We found the growth of human prostate cancer cell line LNCaP was inhibited by 69% by 0.005 U/ml HAL, and PC-3 is inhibited by 81% by 0.01 U/ml HAL. In addition to prostate cancer, three cell lines of human ovarian cancer were tested. The growth of ovarian cancer cell lines SKOV-3 and MA148 were inhibited by 78% and 95% respectively by 0.01 U/ml HAL, and OVCA3 is inhibited by 53% with 0.005 U/ml HAL. In addition to the prostate and ovarian cancer cell lines C6 glioblastoma cells were tested and HAL was found to inhibit growth by 95% at a concentration of 0.01 U/ml.

The results of this widely accepted assay are very encouraging. Clearly, HAL is very effective in controlling the growth of a wide variety of human tumors in vitro and is potentially an effectively anticancer therapeutic.

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 20 25 30

 Xaa Xaa Xaa Xaa Glu Xaa Leu Ala Xaa Xaa Arg Xaa Xaa Xaa Asp Ala
 35 40 45

 Leu Ala Xaa Xaa Xaa Xaa Pro Val Tyr Gly Xaa Ser Thr Gly Phe Gly
 50 55 60

 Ala Leu Ala Xaa Arg His Ile Xaa Xaa Glu Xaa Arg Ala Xaa Leu Gln
 65 70 75 80

 Arg Xaa Xaa Xaa Arg Ser His Ala Ala Gly Met Gly Xaa Xaa Val Glu
 85 90 95

 Arg Glu Val Val Arg Ala Leu Met Phe Leu Arg Xaa Lys Thr Xaa Ala
 100 105 110

 Ser Gly Xaa Thr Gly Val Arg Pro Xaa Val Xaa Xaa Thr Met Xaa Gly
 115 120 125

 Xaa Leu Asn Ala Gly Ile Thr Pro Val Val Xaa Glu Tyr Gly Ser Leu
 130 135 140

 Gly Cys Ser Gly Asp Leu Ala Pro Leu Ser His Cys Ala Leu Xaa Leu
 145 150 155 160

 Met Gly Glu Gly Glu Ala Thr Xaa Xaa Xaa Gly Xaa Xaa Arg Pro Xaa
 165 170 175

 Xaa Glu Leu Xaa Ala Xaa Xaa Gly Xaa Xaa Pro Val Glu Leu Xaa Glu
 180 185 190

 Lys Glu Gly Leu Ala Leu Xaa Asn Gly Thr Asp Gly Met Leu Gly Xaa
 195 200 205

 Leu Xaa Met Ala Leu Ala Asp Leu Xaa Xaa Leu Xaa Xaa Xaa Ala Asp
 210 215 220

 Xaa Thr Ala Ala Xaa Ser Xaa Glu Ala Xaa Leu Gly Thr Asp Xaa Val
 225 230 235 240

 Xaa Xaa Xaa Glu Leu His Xaa Xaa Xaa Arg Pro His Pro Gly Gln Gly
 245 250 255

 Xaa Ser Ala Xaa Asn Met Xaa Xaa Xaa Leu Ala Xaa Ser Xaa Xaa Xaa
 260 265 270

 Xaa Xaa His Xaa Xaa Xaa Xaa Xaa Arg Val Gln Asp Ala Tyr Ser Xaa
 275 280 285

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Arg Cys Xaa Pro Gln Val Xaa Gly Ala Xaa Arg Asp Thr Xaa Xaa His
 290 295 300
 Ala Xaa Leu Val Ala Xaa Arg Glu Leu Ala Xaa Xaa Xaa Asp Asn Pro
 305 310 315 320
 Val Val Leu Pro Xaa Gly Xaa Val Xaa Ser Asn Gly Asn Phe His Gly
 325 330 335
 Ala Pro Val Ala Tyr Val Leu Asp Phe Leu Ala Ile Xaa Xaa Ala Asp
 340 345 350
 Leu Gly Ser Ile Xaa Glu Arg Arg Thr Asp Arg Xaa Leu Asp Xaa Xaa
 355 360 365
 Arg Ser Xaa Xaa Leu Pro Xaa Phe Leu Ala Asp Asp Xaa Gly Val Asp
 370 375 380
 Ser Gly Xaa Met Ile Ala Gln Tyr Thr Gln Ala Xaa Leu Val Xaa Glu
 385 390 395 400
 Xaa Lys Arg Leu Ala Val Pro Ala Ser Xaa Asp Ser Ile Pro Ser Ser
 405 410 415
 Ala Met Gln Glu Asp His Val Ser Xaa Gly Trp Xaa Ala Ala Arg Lys
 420 425 430
 Leu Arg Thr Xaa Val Xaa Asn Leu Xaa Arg Ile Xaa Ala Val Glu Xaa
 435 440 445
 Xaa Xaa Ala Xaa Arg Ala Xaa Xaa Leu Arg Ala Xaa Xaa Xaa Leu Xaa
 450 455 460
 Pro Xaa Pro Ala Xaa Xaa Ala Val Xaa Xaa Xaa Leu Arg Xaa Xaa Xaa
 465 470 475 480
 Ala Xaa Gly Pro Gly Xaa Asp Arg Phe Leu Xaa Xaa Xaa Leu Xaa Ala
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<210> SEQ ID NO 7

<211> LENGTH: 1542

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic expression vector sequence

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 tccgtccgag cacatatcga tgcactagca tccgctgata ccccggttta tggcatttca 180
 accggctttg gcgcggttggc aaccggccac atcgcacccg aggatcgcgc caagctgcag 240
 cgctccctca tccgttccca cgctgctggc atgggtgaac cgggtggagcg cgaagtggtc 300
 cgcgcattga tgttcttgcg tgcaaagacc ctggcttccg gccgcacggg cgttcgcccg 360
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 ttccgcgcag aactgcacga accactgcgc ccgcacccag gccagggccg cagcgcccag 780

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cccggccagg accgcttcct ttccgcagaa ctggaagcag cctatgacct gctggccaat 1500
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<210> SEQ ID NO 8

<211> LENGTH: 286

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide

<400> SEQUENCE: 8

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Asp Asp Val Ile Ala Val Ala Arg His Glu Ala Arg Ile Ser Ile Ser
 20             25             30

Pro Gln Val Leu Glu Glu Leu Ala Ser Val Arg Ala His Ile Asp Ala
 35             40             45

Leu Ala Ser Ala Asp Thr Pro Val Tyr Gly Ile Ser Thr Gly Phe Gly
 50             55             60

Ala Leu Ala Thr Arg His Ile Ala Pro Glu Asp Arg Ala Lys Leu Gln
 65             70             75             80

Arg Ser Leu Ile Arg Ser His Ala Ala Gly Met Gly Glu Pro Val Glu
 85             90             95

Arg Glu Val Val Arg Ala Leu Met Phe Leu Arg Ala Lys Thr Leu Ala
100             105             110

Ser Gly Arg Ser Val Arg Pro Val Val Leu Glu Thr Met Val Gly Met
115             120             125

Leu Asn Ala Gly Ile Thr Pro Val Val Arg Glu Tyr Gly Ser Leu Gly
130             135             140

Cys Ser Gly Asp Leu Ala Pro Leu Ser His Cys Ala Leu Val Leu Met
145             150             155             160

Gly Glu Gly Glu Ala Thr Asp Ala His Gly Asp Ile Arg Pro Val Pro
165             170             175

Glu Leu Phe Ala Glu Ala Gly Leu Thr Pro Val Glu Leu Ala Glu Lys
180             185             190

Glu Gly Leu Ala Leu Val Asn Gly Thr Asp Gly Met Leu Gly Gln Leu
195             200             205

Ile Met Ala Leu Ala Asp Leu Asp Glu Leu Leu Asp Ile Ala Asp Ala
210             215             220

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Thr Ala Ala Met Ser Val Glu Ala Gln Leu Gly Thr Asp Gln Val Phe
 225 230 235 240

Arg Ala Glu Leu His Glu Pro Leu Arg Pro His Pro Gly Gln Gly Arg
 245 250 255

Ser Ala Gln Asn Met Phe Ala Phe Leu Ala Asp Ser Pro Ile Val Ala
 260 265 270

Ser His Arg Glu Gly Asp Gly Arg Val Gln Asp Ala Tyr Ser
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<210> SEQ ID NO 9
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 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 polypeptide

<400> SEQUENCE: 9

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Asp Asp Val Ile Ala Val Ala Arg His Glu Ala Arg Ile Ser Ile Ser
 20 25 30

Pro Gln Val Leu Glu Glu Leu Ala Ser Val Arg Ala His Ile Asp Ala
 35 40 45

Leu Ala Ser Ala Asp Thr Pro Val Tyr Gly Ile Ser Thr Gly Phe Gly
 50 55 60

Ala Leu Ala Thr Arg His Ile Ala Pro Glu Asp Arg Ala Lys Leu Gln
 65 70 75 80

Arg Ser Leu Ile Arg Ser His Ala Ala Gly Met Gly Glu Pro Val Glu
 85 90 95

Arg Glu Val Val Arg Ala Leu Met Phe Leu Arg Ala Lys Thr Leu Ala
 100 105 110

Ser Gly Arg Ser Val Arg Pro Val Val Leu Glu Thr Met Val Gly Met
 115 120 125

Leu Asn Ala Gly Ile Thr Pro Val Val Arg Glu Tyr Gly Ser Leu Gly
 130 135 140

Cys Ser Gly Asp Leu Ala Pro Leu Ser His Cys Ala Leu Val Leu Met
 145 150 155 160

Gly Glu Gly Glu Ala Thr Asp Ala His Gly Asp Ile Arg Pro Val Pro
 165 170 175

Glu Leu Phe Ala Glu Ala Gly Leu Thr Pro Val Glu Leu Ala Glu Lys
 180 185 190

Glu Gly Leu Ala Leu Val Asn Gly Thr Asp Gly Met Leu Gly Gln Leu
 195 200 205

Ile Met Ala Leu Ala Asp Leu Asp Glu Leu Leu Asp Ile Ala Asp Ala
 210 215 220

Thr Ala Ala Met Ser Val Glu Ala Gln Leu Gly Thr Asp Gln Val Phe
 225 230 235 240

Arg Ala Glu Leu His Glu Pro Leu Arg Pro His Pro Gly Gln Gly Arg
 245 250 255

Ser Ala Gln Asn Met Phe Ala Phe Leu Ala Asp Ser Pro Ile Val Ala
 260 265 270

Ser His Arg Glu Gly Asp Gly Arg Val Gln Asp Ala Tyr Ser Leu Arg
 275 280 285

Cys Ser Pro Gln Val Thr Gly Ala Ala Arg Asp Thr Ile Ala His Ala

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290	295	300
Arg Leu Val Ala Thr	Arg Glu Leu Ala Ala	Ile Asp Asn Pro Val
305	310	315 320
Val Leu Pro Ser Gly	Glu Val Thr Ser Asn Gly	Asn Phe His Gly Ala
	325	330 335
Pro Val Ala Tyr Val	Leu Asp Phe Leu Ala	Ile Ala Val Ala Asp Leu
	340	345 350
Gly Ser Ile Ala Glu	Arg Arg Thr Asp Arg	Met Leu Asp Pro Ala Arg
	355	360 365
Ser Arg Asp Leu Pro	Ala Phe Leu Ala Asp	Asp Pro Gly Val Asp Ser
	370	375 380
Gly Met Met Ile Ala	Gln Tyr Thr Gln Ala	Gly Leu Val Ala Glu Asn
385	390	395 400
Lys Arg Leu Ala		

<210> SEQ ID NO 10

<211> LENGTH: 511

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide

<400> SEQUENCE: 10

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	20	25 30
Pro Gln Val Leu Glu	Glu Leu Ala Ser Val	Arg Ala His Ile Asp Ala
	35	40 45
Leu Ala Ser Ala Asp	Thr Pro Val Tyr Gly	Ile Ser Thr Gly Phe Gly
	50	55 60
Ala Leu Ala Thr Arg	His Ile Ala Pro Glu	Asp Arg Ala Lys Leu Gln
	65	70 75 80
Arg Ser Leu Ile Arg	Ser His Ala Ala Gly	Met Gly Glu Pro Val Glu
	85	90 95
Arg Glu Val Val Arg	Ala Leu Met Phe Leu	Arg Ala Lys Thr Leu Ala
	100	105 110
Ser Gly Arg Ser Val	Arg Pro Val Val Leu	Glu Thr Met Val Gly Met
	115	120 125
Leu Asn Ala Gly Ile	Thr Pro Val Val Arg	Glu Tyr Gly Ser Leu Gly
	130	135 140
Cys Ser Gly Asp Leu	Ala Pro Leu Ser His	Cys Ala Leu Val Leu Met
145	150	155 160
Gly Glu Gly Glu Ala	Thr Asp Ala His Gly	Asp Ile Arg Pro Val Pro
	165	170 175
Glu Leu Phe Ala Glu	Ala Gly Leu Thr Pro	Val Glu Leu Ala Glu Lys
	180	185 190
Glu Gly Leu Ala Leu	Val Asn Gly Thr Asp	Gly Met Leu Gly Gln Leu
	195	200 205
Ile Met Ala Leu Ala	Asp Leu Asp Glu Leu	Leu Asp Ile Ala Asp Ala
	210	215 220
Thr Ala Ala Met Ser	Val Glu Ala Gln Leu	Gly Thr Asp Gln Val Phe
225	230	235 240
Arg Ala Glu Leu His	Glu Pro Leu Arg Pro	His Pro Gly Gln Gly Arg

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Ser	Ala	Gln	Asn	Met	Phe	Ala	Phe	Leu	Ala	Asp	Ser	Pro	Ile	Val	Ala
			260					265					270		
Ser	His	Arg	Glu	Gly	Asp	Gly	Arg	Val	Gln	Asp	Ala	Tyr	Ser	Leu	Arg
		275					280					285			
Cys	Ser	Pro	Gln	Val	Thr	Gly	Ala	Ala	Arg	Asp	Thr	Ile	Ala	His	Ala
	290					295					300				
Arg	Leu	Val	Ala	Thr	Arg	Glu	Leu	Ala	Ala	Ala	Ile	Asp	Asn	Pro	Val
305						310					315				320
Val	Leu	Pro	Ser	Gly	Glu	Val	Thr	Ser	Asn	Gly	Asn	Phe	His	Gly	Ala
				325					330					335	
Pro	Val	Ala	Tyr	Val	Leu	Asp	Phe	Leu	Ala	Ile	Ala	Val	Ala	Asp	Leu
			340					345					350		
Gly	Ser	Ile	Ala	Glu	Arg	Arg	Thr	Asp	Arg	Met	Leu	Asp	Pro	Ala	Arg
		355					360					365			
Ser	Arg	Asp	Leu	Pro	Ala	Phe	Leu	Ala	Asp	Asp	Pro	Gly	Val	Asp	Ser
	370					375					380				
Gly	Met	Met	Ile	Ala	Gln	Tyr	Thr	Gln	Ala	Gly	Leu	Val	Ala	Glu	Asn
385				390						395					400
Lys	Arg	Leu	Ala	Val	Pro	Ala	Val	Asp	Ser	Ile	Pro	Ser	Ser	Ala	Met
			405						410					415	
Gln	Glu	Asp	His	Val	Ser	Leu	Gly	Trp	His	Ala	Ala	Arg	Lys	Leu	Pro
		420						425					430		
Thr	Ser	Val	Ala	Asn	Leu	Arg	Arg	Ile	Leu	Ala	Val	Glu	Met	Leu	Ile
		435					440					445			
Ala	Gly	Arg	Ala	Leu	Asp	Leu	Arg	Ala	Pro	Leu	Lys	Pro	Gly	Pro	Ala
	450					455					460				
Thr	Gly	Ala	Val	Leu	Glu	Val	Leu	Arg	Ser	Lys	Val	Ala	Gly	Pro	Gly
465				470						475				480	
Gln	Asp	Arg	Phe	Leu	Ser	Ala	Glu	Leu	Glu	Ala	Ala	Tyr	Asp	Leu	Leu
			485						490					495	
Ala	Asn	Gly	Ser	Val	His	Lys	Ala	Leu	Glu	Ala	His	Leu	Pro	Glu	
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<210> SEQ ID NO 11
 <211> LENGTH: 511
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Formula
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<221> NAME/KEY: MOD_RES
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<223> OTHER INFORMATION: Variable amino acid
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<223> OTHER INFORMATION: Variable amino acid
<221> NAME/KEY: MOD_RES
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<223> OTHER INFORMATION: Variable amino acid
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<223> OTHER INFORMATION: Variable amino acid

<400> SEQUENCE: 11

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Ser Gly Xaa Thr Ala
 1           5           10          15
Xaa Asp Val Xaa Ala Val Ala Arg His Xaa Ala Arg Xaa Xaa Xaa Ser
          20           25           30
Xaa Xaa Xaa Xaa Glu Xaa Leu Ala Xaa Xaa Arg Xaa Xaa Xaa Asp Ala
          35           40           45
Leu Ala Xaa Xaa Xaa Xaa Pro Val Tyr Gly Xaa Ser Thr Gly Phe Gly
          50           55           60
Ala Leu Ala Xaa Arg His Ile Xaa Xaa Glu Xaa Arg Ala Xaa Leu Gln
          65           70           75           80
Arg Xaa Xaa Xaa Arg Ser His Ala Ala Gly Met Gly Xaa Xaa Val Glu
          85           90           95
Arg Glu Val Val Arg Ala Leu Met Phe Leu Arg Xaa Lys Thr Xaa Ala
          100          105          110
Ser Gly Xaa Xaa Val Arg Pro Xaa Val Xaa Xaa Thr Met Xaa Gly Xaa
          115          120          125
Leu Asn Ala Gly Ile Thr Pro Val Val Xaa Glu Tyr Gly Ser Leu Gly
          130          135          140
Cys Ser Gly Asp Leu Ala Pro Leu Ser His Cys Ala Leu Val Leu Met
          145          150          155          160
Gly Glu Gly Glu Ala Thr Xaa Xaa Xaa Gly Xaa Xaa Arg Pro Xaa Xaa
          165          170          175
Glu Leu Xaa Ala Xaa Xaa Gly Xaa Xaa Pro Val Glu Leu Xaa Glu Lys
          180          185          190
Glu Gly Leu Ala Leu Xaa Asn Gly Thr Asp Gly Met Leu Gly Xaa Leu
          195          200          205
Xaa Met Ala Leu Ala Asp Leu Xaa Xaa Leu Xaa Xaa Xaa Ala Asp Xaa
          210          215          220
Thr Ala Ala Xaa Ser Xaa Glu Ala Xaa Leu Gly Thr Asp Xaa Val Xaa
          225          230          235          240
Xaa Xaa Glu Leu His Xaa Xaa Xaa Arg Pro His Pro Gly Gln Gly Xaa
          245          250          255
Ser Ala Xaa Asn Met Xaa Xaa Xaa Leu Ala Xaa Ser Xaa Xaa Xaa Xaa
          260          265          270
Xaa His Xaa Xaa Xaa Xaa Xaa Arg Val Gln Asp Ala Tyr Ser Xaa Arg
          275          280          285
Cys Xaa Pro Gln Val Xaa Gly Ala Xaa Arg Asp Thr Xaa Xaa His Ala

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290	295	300
Xaa Leu Val Ala Xaa Arg Glu Leu Ala Xaa Xaa Xaa Asp Asn Pro Val 305	310	315
Val Leu Pro Xaa Gly Xaa Val Xaa Ser Asn Gly Asn Phe His Gly Ala 325	330	335
Pro Val Ala Tyr Val Leu Asp Phe Leu Ala Ile Xaa Xaa Ala Asp Leu 340	345	350
Gly Ser Ile Xaa Glu Arg Arg Thr Asp Arg Xaa Leu Asp Xaa Xaa Arg 355	360	365
Ser Xaa Xaa Leu Pro Xaa Phe Leu Ala Asp Asp Xaa Gly Val Asp Ser 370	375	380
Gly Xaa Met Ile Ala Gln Tyr Thr Gln Ala Xaa Leu Val Xaa Glu Xaa 385	390	395
Lys Arg Leu Ala Val Pro Ala Xaa Asp Ser Ile Pro Ser Ser Ala Met 405	410	415
Gln Glu Asp His Val Ser Xaa Gly Trp Xaa Ala Ala Arg Lys Leu Xaa 420	425	430
Thr Xaa Val Xaa Asn Leu Xaa Arg Ile Xaa Ala Val Glu Xaa Xaa Xaa 435	440	445
Ala Xaa Arg Ala Xaa Xaa Leu Arg Ala Xaa Xaa Xaa Xaa Xaa Pro Ala 450	455	460
Xaa Xaa Ala Val Xaa Xaa Xaa Leu Arg Xaa Xaa Xaa Ala Gly Pro Gly 465	470	475
Gln Asp Arg Phe Leu Xaa Xaa Xaa Leu Xaa Ala Ala Xaa Xaa Xaa Xaa 485	490	495
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa Xaa Xaa Xaa 500	505	510

<210> SEQ ID NO 12

<211> LENGTH: 1536

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic expression vector sequence

<400> SEQUENCE: 12

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atggcttccg ctcctcaaat aacacttggc ctaagtggcg caaccgcaga cgacgttatc    60
gccgttgccc gccacgaagc ccgcatcagc atttctccgc aagtacttga ggaactggct    120
tccgtccgag cacatatcga tgcactagca tccgctgata ccccggttta tggcatttca    180
accggctttg gcgcgttggc aaccgcacc atcgcacccg aggatcgcg caagctgcag    240
cgctccctca tccgttccca cgctgctggc atgggtgaac cggtgagcg cgaagtggtc    300
cgcgcattga tgttcttgcg tgcaaagacc ctggcttccg gccgcagcgt tcgcccggtt    360
gtccttgaga ccatggtcgg catgctcaat gcaggcatca ctccggtagt ccggaatac    420
ggttcaactg gctgctccgg tgacttggct ccgctgtcgc actgcgcat agtgctgatg    480
ggcgagggcg aagccaccga tgcccacggc gacatccgcc cggtagcga actgttcgcc    540
gaggccggat tgaccctgt cgaactggca gaaaaggaag gcctggctct ggtcaacggc    600
accgacggca tgctcggcca gctgatcatg gcattggcgg acctcgatga gctgctggac    660
atcgccgatg ccaccgccgc catgagcgtt gaagcccagc tgggcaccga tcaggtattc    720
cgcgcagaac tgacgaacc actgcgccc caccagggc agggccgcag cgcccagaac    780
atgttcgcct tcctggccga ctgcgaatt gttgcctcgc atcgcgagg agacggccga    840

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gtgcaggatg cctactcgtc gcggttgctc cgcaggtea cggcgccgc ccgagacacc 900
attgctcatg cccgcctggt cggcaccgc gaactggctg cggccattga caaccctgtg 960
gtgctgcca gggcgaaat gacttccaac ggcaacttcc acggcgcacc ggtagcctac 1020
gtgctggact tccttgccat cggcgtggcc gacctcggct ctatcgccga gcgcccacc 1080
gaccgcatgc tcgaccagc ccgctcccgc gacctgcgg cattcctggc cgacgatccg 1140
ggtgtggact cgggcatgat gatcgcccag tacactcagg ccggcttggg ggcagaaaac 1200
aagcggctgg cagttcctgc agttgactcc atcccatcct cggccatgca ggaagaccac 1260
gtttccctgg gctggcatgc ggcgcgcaag ctgccgacct cggtagcgaa cctccgccc 1320
attctcgcag tggaaatgct gattgccggc cgcgccctgg acctgcgggc cccattgaag 1380
cctggtccag cgaccggtgc ggtgctttaa gtattgcgca gcaaggttgc aggccccggc 1440
caggaccgct tcctttccgc agaactgaa gcagcctatg acctgctggc caatggctcg 1500
gtgcataagg ccctcgaagc tcacctgcct gaataa 1536

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<210> SEQ ID NO 13

<211> LENGTH: 30

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 13

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cgcgttcagg acgcatactc cgttcgtctg 30

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<210> SEQ ID NO 14

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 14

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gcccattgaa acgtggtctt cctg 24

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<210> SEQ ID NO 15

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 15

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atcatcatgc ccgagtccac a 21

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<210> SEQ ID NO 16

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 16

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gccatcagga agaccagtt t 21

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<210> SEQ ID NO 17

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<211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> SEQUENCE: 17

atgcaggaag accacgtttc 20

<210> SEQ ID NO 18
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> SEQUENCE: 18

atcgaggtcc gccaatgcca t 21

<210> SEQ ID NO 19
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> SEQUENCE: 19

accggagcag cccagtga 18

<210> SEQ ID NO 20
 <211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> SEQUENCE: 20

tgcttgaagt attgcgccag 20

<210> SEQ ID NO 21
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> SEQUENCE: 21

gatcctcggg tgcgatgt 18

<210> SEQ ID NO 22
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> SEQUENCE: 22

atgctgatcg ggcttcgt 18

<210> SEQ ID NO 23
 <211> LENGTH: 27

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<212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> SEQUENCE: 23

atttgattca tatggcttcc gctcctc 27

<210> SEQ ID NO 24
 <211> LENGTH: 28
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> SEQUENCE: 24

atcttggatc cgaacatggt gcggtgca 28

<210> SEQ ID NO 25
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> SEQUENCE: 25

agcaccagat cgatgcac 18

<210> SEQ ID NO 26
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> SEQUENCE: 26

tggcatgggt gaaccggt 18

<210> SEQ ID NO 27
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> SEQUENCE: 27

atcagcgttg aagcccag 18

<210> SEQ ID NO 28
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> SEQUENCE: 28

acgtgctgga cttccttg 18

<210> SEQ ID NO 29
 <211> LENGTH: 18
 <212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 oligonucleotide

 <400> SEQUENCE: 29

 gtgcataagg ccctcgaa 18

 <210> SEQ ID NO 30
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 oligonucleotide

 <400> SEQUENCE: 30

 gagcttcgag ggccttat 18

 <210> SEQ ID NO 31
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 oligonucleotide

 <400> SEQUENCE: 31

 cgagcaacgc agcgagta 18

 <210> SEQ ID NO 32
 <211> LENGTH: 13
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 peptide

 <400> SEQUENCE: 32

 Met Ala Leu Ala Asp Leu Asp Glu Leu Leu Asp Glu Ala
 1 5 10

 <210> SEQ ID NO 33
 <211> LENGTH: 12
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 peptide

 <400> SEQUENCE: 33

 Met Gly Glu Pro Val Glu Arg Glu Val Leu Arg Ala
 1 5 10

 <210> SEQ ID NO 34
 <211> LENGTH: 509
 <212> TYPE: PRT
 <213> ORGANISM: Pseudomonas putida

 <400> SEQUENCE: 34

 Thr Glu Leu Thr Leu Lys Pro Gly Thr Leu Thr Leu Ala Gln Leu Arg
 1 5 10 15

 Ala Ile His Ala Ala Pro Val Arg Leu Gln Leu Asp Ala Ser Ala Ala
 20 25 30

 Pro Ala Ile Asp Ala Ser Val Ala Cys Val Glu Gln Ile Ile Ala Glu
 35 40 45

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Asp Arg Thr Ala Tyr Gly Ile Asn Thr Gly Phe Gly Leu Leu Ala Ser
 50 55 60

Thr Arg Ile Ala Ser His Asp Leu Glu Asn Leu Gln Arg Ser Leu Val
 65 70 75 80

Leu Ser His Ala Ala Gly Ile Gly Ala Pro Leu Asp Asp Asp Leu Val
 85 90 95

Arg Leu Ile Met Val Leu Lys Ile Asn Ser Leu Ser Arg Gly Phe Ser
 100 105 110

Gly Ile Arg Arg Lys Val Ile Asp Ala Leu Ile Ala Leu Val Asn Ala
 115 120 125

Glu Val Tyr Pro His Ile Pro Leu Lys Gly Ser Val Gly Ala Ser Gly
 130 135 140

Asp Leu Ala Pro Leu Ala Thr Met Ser Leu Val Leu Leu Gly Glu Gly
 145 150 155 160

Lys Ala Arg Tyr Lys Gly Gln Trp Leu Ser Ala Thr Glu Ala Leu Ala
 165 170 175

Val Ala Gly Leu Glu Pro Leu Thr Leu Ala Ala Lys Glu Gly Leu Ala
 180 185 190

Leu Leu Asn Gly Thr Gln Ala Ser Thr Ala Tyr Ala Leu Arg Gly Leu
 195 200 205

Phe Tyr Ala Glu Asp Leu Tyr Ala Ala Ala Ile Ala Cys Gly Gly Leu
 210 215 220

Ser Val Glu Ala Val Leu Gly Ser Arg Ser Pro Phe Asp Ala Arg Ile
 225 230 235 240

His Glu Ala Arg Gly Gln Arg Gly Gln Ile Asp Thr Ala Ala Cys Phe
 245 250 255

Arg Asp Leu Leu Gly Asp Ser Ser Glu Val Ser Leu Ser His Lys Asn
 260 265 270

Cys Asp Lys Val Gln Asp Pro Tyr Ser Leu Arg Cys Gln Pro Gln Val
 275 280 285

Met Gly Ala Cys Leu Thr Gln Leu Arg Gln Ala Ala Glu Val Leu Gly
 290 295 300

Ile Glu Ala Asn Ala Val Ser Asp Asn Pro Leu Val Phe Ala Ala Glu
 305 310 315 320

Gly Asp Val Ile Ser Gly Gly Asn Phe His Ala Glu Pro Val Ala Met
 325 330 335

Ala Ala Asp Asn Leu Ala Leu Ala Ile Ala Glu Ile Gly Ser Leu Ser
 340 345 350

Glu Arg Arg Ile Ser Leu Met Met Asp Lys His Met Ser Gln Leu Pro
 355 360 365

Pro Phe Leu Val Glu Asn Gly Gly Val Asn Ser Gly Phe Met Ile Ala
 370 375 380

Gln Val Thr Ala Ala Ala Leu Ala Ser Glu Asn Lys Ala Leu Ser His
 385 390 395 400

Pro His Ser Val Asp Ser Leu Pro Thr Ser Ala Asn Gln Glu Asp His
 405 410 415

Val Ser Met Ala Pro Ala Ala Gly Lys Arg Leu Trp Glu Met Ala Glu
 420 425 430

Asn Thr Arg Gly Val Pro Ala Ile Glu Trp Leu Gly Ala Cys Gln Gly
 435 440 445

Leu Asp Leu Arg Lys Gly Leu Lys Thr Ser Ala Lys Leu Glu Lys Ala
 450 455 460

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Arg Gln Ala Leu Arg Ser Glu Val Ala His Tyr Asp Arg Asp Arg Phe
 465 470 475 480
 Phe Ala Pro Asp Ile Glu Lys Ala Val Glu Leu Leu Ala Lys Gly Ser
 485 490 495
 Leu Thr Gly Leu Leu Pro Ala Gly Val Leu Pro Ser Leu
 500 505

 <210> SEQ ID NO 35
 <211> LENGTH: 511
 <212> TYPE: PRT
 <213> ORGANISM: Rhizobium meliloti

 <400> SEQUENCE: 35
 Met Thr Val Ile Leu Arg Pro Gly Ser Val Pro Leu Ser Asp Leu Glu
 1 5 10 15
 Thr Ile Tyr Trp Thr Gly Ala Pro Ala Arg Leu Asp Ala Ala Phe Asp
 20 25 30
 Ala Gly Ile Ala Lys Ala Ala Ala Arg Ile Ala Glu Ile Val Ala Gly
 35 40 45
 Asn Ala Pro Val Tyr Gly Ile Asn Thr Gly Phe Gly Lys Leu Ala Ser
 50 55 60
 Ile Lys Ile Asp Ser Ser Asp Val Ala Thr Leu Gln Arg Asn Leu Ile
 65 70 75 80
 Leu Ser His Cys Cys Gly Val Gly Gln Pro Leu Thr Glu Asp Ile Val
 85 90 95
 Arg Leu Ile Met Ala Leu Lys Leu Ile Ser Leu Gly Arg Gly Ala Ser
 100 105 110
 Gly Val Arg Leu Glu Leu Val Arg Leu Ile Glu Ala Met Leu Asp Lys
 115 120 125
 Gly Val Ile Pro Leu Ile Pro Glu Lys Gly Ser Val Gly Ala Ser Gly
 130 135 140
 Asp Leu Ala Pro Leu Ala His Met Ala Ala Val Met Met Gly His Gly
 145 150 155 160
 Glu Ala Phe Phe Ala Gly Glu Arg Met Lys Gly Asp Ala Ala Leu Lys
 165 170 175
 Ala Ala Gly Leu Ser Pro Val Thr Leu Ala Ala Lys Glu Gly Leu Ala
 180 185 190
 Leu Ile Asn Gly Thr Gln Val Ser Thr Ala Leu Ala Leu Ala Gly Leu
 195 200 205
 Phe Arg Ala His Arg Ala Gly Gln Ala Ala Leu Ile Thr Gly Ala Leu
 210 215 220
 Ser Thr Asp Ala Ala Met Gly Ser Ser Ala Pro Phe His Pro Asp Ile
 225 230 235 240
 Gln His Cys Ala Ala Ile Arg Ala Arg Ser Thr Arg Ala Ala Ala Leu
 245 250 255
 Arg Gln Leu Leu Thr Gly Ser Pro Ile Arg Gln Ser His Ile Glu Gly
 260 265 270
 Asp Glu Arg Val Gln Asp Pro Tyr Cys Ile Arg Cys Gln Pro Gln Val
 275 280 285
 Asp Gly Ala Cys Leu Asp Leu Leu Arg Ser Val Ala Ala Thr Leu Thr
 290 295 300
 Ile Glu Ala Asn Ala Val Thr Asp Asn Pro Leu Val Leu Ser Asp Asn
 305 310 315 320
 Ser Val Val Ser Gly Gly Asn Phe His Ala Glu Pro Val Ala Phe Ala
 325 330 335

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Ala Asp Gln Ile Ala Leu Ala Val Cys Glu Ile Gly Ala Ile Ser Gln
 340 345 350

Arg Arg Ile Ala Leu Leu Val Asp Pro Ala Leu Ser Leu Arg Leu Pro
 355 360 365

Ala Phe Leu Ala Lys Lys Pro Gly Leu Asn Ser Gly Leu Met Ile Ala
 370 375 380

Glu Val Thr Ser Ala Ala Leu Met Ser Glu Asn Lys Gln Leu Ser His
 385 390 395 400

Pro Ala Ser Val Asp Ser Thr Pro Thr Ser Ala Asn Gln Glu Asp His
 405 410 415

Val Ser Met Ala Cys His Gly Ala Arg Arg Leu Leu Gln Met Thr Glu
 420 425 430

Asn Leu Phe Ser Ile Ile Gly Ile Glu Ala Leu Ala Ala Val Gln Gly
 435 440 445

Ile Glu Phe Arg Ala Pro Leu Thr Thr Ser Pro Glu Leu Gln Lys Ala
 450 455 460

Ala Ala Ala Val Arg Gly Val Ser Ser Ser Ile Glu Glu Asp Arg Tyr
 465 470 475 480

Met Ala Asp Asp Leu Lys Ala Ala Gly Asp Leu Val Ala Ser Gly Arg
 485 490 495

Leu Ala Ala Ala Val Ser Ala Gly Ile Leu Pro Lys Leu Glu Asn
 500 505 510

<210> SEQ ID NO 36
 <211> LENGTH: 657
 <212> TYPE: PRT
 <213> ORGANISM: Mus sp.

<400> SEQUENCE: 36

Met Pro Arg Tyr Thr Val His Val Arg Gly Glu Trp Leu Ala Val Pro
 1 5 10 15

Cys Gln Asp Gly Lys Leu Thr Val Gly Trp Leu Gly Arg Glu Ala Val
 20 25 30

Arg Arg Tyr Met Lys Asn Lys Pro Asp Asn Gly Gly Phe Thr Ser Val
 35 40 45

Asp Glu Val Gln Phe Leu Val His Arg Cys Lys Gly Leu Gly Leu Leu
 50 55 60

Asp Asn Glu Asp Glu Leu Glu Val Ala Leu Glu Asp Asn Glu Phe Val
 65 70 75 80

Glu Val Val Ile Glu Gly Asp Val Met Ser Pro Asp Phe Ile Pro Ser
 85 90 95

Gln Pro Glu Gly Val Phe Leu Tyr Ser Lys Tyr Arg Glu Pro Glu Lys
 100 105 110

Tyr Ile Ala Leu Asp Gly Asp Ser Leu Ser Thr Glu Asp Leu Val Asn
 115 120 125

Leu Gly Lys Gly Arg Tyr Lys Ile Lys Leu Thr Ser Ile Ala Glu Lys
 130 135 140

Lys Val Gln Gln Ser Arg Glu Val Ile Asp Ser Ile Ile Lys Glu Arg
 145 150 155 160

Thr Val Val Tyr Gly Ile Thr Thr Gly Phe Gly Lys Phe Ala Arg Thr
 165 170 175

Val Ile Pro Ala Asn Lys Leu Gln Glu Leu Gln Val Asn Leu Val Arg
 180 185 190

Ser His Ser Ser Gly Val Gly Lys Pro Leu Ser Pro Glu Arg Cys Arg

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195					200					205					
Met	Leu	Leu	Ala	Leu	Arg	Ile	Asn	Val	Leu	Ala	Lys	Gly	Tyr	Ser	Gly
	210					215					220				
Ile	Ser	Leu	Glu	Thr	Leu	Lys	Gln	Val	Ile	Glu	Ala	Phe	Asn	Ala	Ser
225					230					235					240
Cys	Leu	Ser	Tyr	Val	Pro	Glu	Lys	Gly	Thr	Val	Gly	Ala	Ser	Gly	Asp
				245					250					255	
Leu	Ala	Pro	Leu	Ser	His	Leu	Ala	Leu	Gly	Leu	Ile	Gly	Glu	Gly	Lys
			260					265					270		
Met	Trp	Ser	Pro	Lys	Ser	Gly	Trp	Ala	Asp	Ala	Lys	Tyr	Val	Leu	Glu
		275					280					285			
Ala	His	Gly	Leu	Lys	Pro	Ile	Val	Leu	Lys	Pro	Lys	Glu	Gly	Leu	Ala
	290					295					300				
Leu	Ile	Asn	Gly	Thr	Gln	Met	Ile	Thr	Ser	Leu	Gly	Cys	Glu	Ala	Leu
305					310					315					320
Glu	Arg	Ala	Ser	Ala	Ile	Ala	Arg	Gln	Ala	Asp	Ile	Val	Ala	Ala	Leu
				325					330					335	
Thr	Leu	Glu	Val	Leu	Lys	Gly	Thr	Thr	Lys	Ala	Phe	Asp	Thr	Asp	Ile
			340					345					350		
His	Ala	Val	Arg	Pro	His	Arg	Gly	Gln	Ile	Glu	Val	Ala	Phe	Arg	Phe
		355					360					365			
Arg	Ser	Leu	Leu	Asp	Ser	Asp	His	His	Pro	Ser	Glu	Ile	Ala	Glu	Ser
	370					375					380				
His	Arg	Phe	Cys	Asp	Arg	Val	Gln	Asp	Ala	Tyr	Thr	Leu	Arg	Cys	Cys
385					390					395					400
Pro	Gln	Val	His	Gly	Val	Val	Asn	Asp	Thr	Ile	Ala	Phe	Val	Lys	Asp
				405					410					415	
Ile	Ile	Thr	Thr	Glu	Leu	Asn	Ser	Ala	Thr	Asp	Asn	Pro	Met	Val	Phe
			420					425					430		
Ala	Ser	Arg	Gly	Glu	Thr	Ile	Ser	Gly	Gly	Asn	Phe	His	Gly	Glu	Tyr
		435					440					445			
Pro	Ala	Lys	Ala	Leu	Asp	Tyr	Leu	Ala	Ile	Gly	Val	His	Glu	Leu	Ala
	450					455					460				
Ala	Ile	Ser	Glu	Arg	Arg	Ile	Glu	Arg	Leu	Cys	Asn	Pro	Ser	Leu	Ser
465					470					475					480
Glu	Leu	Pro	Ala	Phe	Leu	Val	Ala	Glu	Gly	Gly	Leu	Asn	Ser	Gly	Phe
				485					490					495	
Met	Ile	Ala	His	Cys	Thr	Ala	Ala	Ala	Leu	Val	Ser	Glu	Ser	Lys	Ala
			500					505					510		
Leu	Cys	His	Pro	Ser	Ser	Val	Asp	Ser	Leu	Ser	Thr	Ser	Ala	Ala	Thr
		515					520					525			
Glu	Asp	His	Val	Ser	Met	Gly	Gly	Trp	Ala	Ala	Arg	Lys	Ala	Leu	Arg
	530					535					540				
Val	Val	Glu	His	Val	Glu	Gln	Val	Leu	Ala	Ile	Glu	Leu	Leu	Ala	Ala
545					550					555					560
Cys	Gln	Gly	Ile	Glu	Phe	Leu	Arg	Pro	Leu	Lys	Thr	Thr	Thr	Pro	Leu
				565					570					575	
Glu	Lys	Val	Tyr	Asp	Leu	Val	Arg	Ser	Val	Val	Arg	Pro	Trp	Ile	Lys
			580					585					590		
Asp	Arg	Phe	Met	Ala	Pro	Asp	Ile	Glu	Ala	Ala	His	Arg	Leu	Leu	Leu
		595					600					605			
Asp	Gln	Lys	Val	Trp	Glu	Val	Ala	Ala	Pro	Tyr	Ile	Glu	Lys	Tyr	Arg
	610					615					620				

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Met Glu His Ile Pro Glu Ser Arg Pro Leu Ser Pro Thr Ala Phe Ser
 625 630 635 640

Leu Glu Ser Leu Arg Lys Asn Ser Ala Thr Ile Pro Glu Ser Asp Asp
 645 650 655

Leu

<210> SEQ ID NO 37
 <211> LENGTH: 657
 <212> TYPE: PRT
 <213> ORGANISM: Rattus sp.

<400> SEQUENCE: 37

Met Pro Arg Tyr Thr Val His Val Arg Gly Glu Trp Leu Ala Val Pro
 1 5 10 15

Cys Gln Asp Gly Lys Leu Ser Val Gly Trp Leu Gly Arg Glu Ala Val
 20 25 30

Arg Arg Tyr Met Lys Asn Lys Pro Asp Asn Gly Gly Phe Thr Ser Val
 35 40 45

Asp Glu Val Arg Phe Leu Val Arg Arg Cys Lys Gly Leu Gly Leu Leu
 50 55 60

Asp Asn Glu Asp Leu Leu Glu Val Ala Leu Glu Asp Asn Glu Phe Val
 65 70 75 80

Glu Val Val Ile Glu Gly Asp Val Met Ser Pro Asp Phe Ile Pro Ser
 85 90 95

Gln Pro Glu Gly Val Phe Leu Tyr Ser Lys Tyr Arg Glu Pro Glu Lys
 100 105 110

Tyr Ile Ala Leu Asp Gly Asp Ser Leu Ser Thr Glu Asp Leu Val Asn
 115 120 125

Leu Gly Lys Gly His Tyr Lys Ile Lys Leu Thr Ser Ile Ala Glu Lys
 130 135 140

Lys Val Gln Gln Ser Arg Glu Val Ile Asp Ser Ile Ile Lys Glu Arg
 145 150 155 160

Thr Val Val Tyr Gly Ile Thr Thr Gly Phe Gly Lys Phe Ala Arg Thr
 165 170 175

Val Ile Pro Ala Asn Lys Leu Gln Glu Leu Gln Val Asn Leu Val Arg
 180 185 190

Ser His Ser Ser Gly Val Gly Lys Pro Leu Ser Pro Glu Arg Cys Arg
 195 200 205

Met Leu Leu Ala Leu Arg Ile Asn Val Leu Ala Lys Gly Tyr Ser Gly
 210 215 220

Ile Ser Leu Glu Thr Leu Lys Gln Val Ile Glu Val Phe Asn Ala Ser
 225 230 235 240

Cys Leu Ser Tyr Val Pro Glu Lys Gly Thr Val Gly Ala Ser Gly Asp
 245 250 255

Leu Ala Pro Leu Ser His Leu Ala Leu Gly Leu Ile Gly Glu Gly Lys
 260 265 270

Met Trp Ser Pro Lys Ser Gly Trp Ala Asp Ala Lys Tyr Val Leu Glu
 275 280 285

Ala His Gly Leu Lys Pro Ile Val Leu Lys Pro Lys Glu Gly Leu Ala
 290 295 300

Leu Ile Asn Gly Thr Gln Met Ile Thr Ser Leu Gly Cys Glu Ala Val
 305 310 315 320

Glu Arg Ala Ser Ala Ile Ala Arg Gln Ala Asp Ile Val Ala Ala Leu
 325 330 335

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Thr Leu Glu Val Leu Lys Gly Thr Thr Lys Ala Phe Asp Thr Asp Ile
 340 345 350
 His Ala Val Arg Pro His Arg Gly Gln Ile Glu Val Ala Phe Arg Phe
 355 360 365
 Arg Ser Leu Leu Asp Ser Asp His His Pro Ser Glu Ile Ala Glu Ser
 370 375 380
 His Arg Phe Cys Asp Arg Val Gln Asp Ala Tyr Thr Leu Arg Cys Cys
 385 390 395 400
 Pro Gln Val His Gly Val Val Asn Asp Thr Ile Ala Phe Val Lys Asp
 405 410 415
 Ile Ile Thr Thr Glu Leu Asn Ser Ala Thr Asp Asn Pro Met Val Phe
 420 425 430
 Ala Ser Arg Gly Glu Thr Ile Ser Gly Gly Asn Phe His Gly Glu Tyr
 435 440 445
 Pro Ala Lys Ala Leu Asp Tyr Leu Ala Ile Gly Val His Glu Leu Ala
 450 455 460
 Ala Ile Ser Glu Arg Arg Ile Glu Arg Leu Cys Asn Pro Ser Leu Ser
 465 470 475 480
 Glu Leu Pro Ala Phe Leu Val Ala Glu Gly Gly Leu Asn Ser Gly Phe
 485 490 495
 Met Ile Ala His Cys Thr Ala Ala Ala Leu Val Ser Glu Ser Lys Ala
 500 505 510
 Leu Cys His Pro Ser Ser Val Asp Ser Leu Ser Thr Ser Ala Ala Thr
 515 520 525
 Glu Asp His Val Ser Met Gly Gly Trp Ala Ala Arg Lys Ala Leu Arg
 530 535 540
 Val Ile Glu His Val Glu Gln Val Leu Ala Ile Glu Leu Leu Ala Ala
 545 550 555 560
 Cys Gln Gly Ile Glu Phe Leu Arg Pro Leu Lys Thr Thr Thr Pro Leu
 565 570 575
 Glu Lys Val Tyr Asp Leu Val Arg Ser Val Val Arg Pro Trp Ile Lys
 580 585 590
 Asp Arg Phe Met Ala Pro Asp Ile Glu Ala Ala His Arg Leu Leu Leu
 595 600 605
 Asp Gln Lys Val Trp Glu Val Ala Ala Pro Tyr Ile Glu Lys Tyr Arg
 610 615 620
 Met Glu His Ile Pro Glu Ser Arg Pro Leu Ser Pro Thr Ala Phe Ser
 625 630 635 640
 Leu Glu Ser Leu Arg Lys Asn Ser Ala Thr Ile Pro Glu Ser Asp Asp
 645 650 655
 Leu

<210> SEQ ID NO 38

<211> LENGTH: 635

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 38

Met Pro Arg Tyr Thr Val His Val Arg Gly Glu Trp Leu Ala Val Pro
 1 5 10 15
 Cys Gln Asp Ala Gln Leu Thr Val Gly Trp Leu Gly Arg Glu Ala Val
 20 25 30
 Arg Arg Tyr Ile Lys Asn Lys Pro Asp Asn Gly Gly Phe Thr Ser Val
 35 40 45

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Asp	Asp	Ala	His	Phe	Leu	Val	Arg	Arg	Cys	Lys	Gly	Leu	Gly	Leu	Leu
	50					55					60				
Asp	Asn	Glu	Asp	Arg	Leu	Glu	Val	Ala	Leu	Glu	Asn	Asn	Glu	Phe	Val
65					70					75					80
Glu	Val	Val	Ile	Glu	Gly	Asp	Ala	Met	Ser	Pro	Asp	Phe	Ile	Pro	Ser
				85					90					95	
Gln	Pro	Glu	Gly	Val	Tyr	Leu	Tyr	Ser	Lys	Tyr	Arg	Glu	Pro	Glu	Lys
			100					105					110		
Tyr	Ile	Glu	Leu	Asp	Gly	Asp	Arg	Leu	Thr	Thr	Glu	Asp	Leu	Val	Asn
		115					120					125			
Leu	Gly	Lys	Gly	Arg	Tyr	Lys	Ile	Lys	Leu	Thr	Pro	Thr	Ala	Glu	Lys
	130					135					140				
Arg	Val	Gln	Lys	Ser	Arg	Glu	Val	Ile	Asp	Ser	Ile	Ile	Lys	Glu	Lys
145					150					155					160
Thr	Val	Val	Tyr	Gly	Ile	Thr	Thr	Gly	Phe	Gly	Lys	Phe	Ala	Arg	Thr
				165					170					175	
Val	Ile	Pro	Ile	Asn	Lys	Leu	Gln	Glu	Leu	Gln	Val	Asn	Leu	Val	Arg
			180					185					190		
Ser	His	Ser	Ser	Gly	Val	Gly	Lys	Pro	Leu	Ser	Pro	Glu	Arg	Cys	Arg
		195					200					205			
Met	Leu	Leu	Ala	Leu	Arg	Ile	Asn	Val	Leu	Ala	Lys	Gly	Tyr	Ser	Gly
	210					215					220				
Ile	Ser	Leu	Glu	Thr	Leu	Lys	Gln	Val	Ile	Glu	Met	Phe	Asn	Ala	Ser
225					230					235					240
Cys	Leu	Pro	Tyr	Val	Pro	Glu	Lys	Gly	Thr	Val	Gly	Ala	Ser	Gly	Asp
				245					250					255	
Leu	Ala	Pro	Leu	Ser	His	Leu	Ala	Leu	Gly	Leu	Val	Gly	Glu	Gly	Lys
			260					265					270		
Met	Trp	Ser	Pro	Lys	Ser	Gly	Trp	Ala	Asp	Ala	Lys	Tyr	Val	Leu	Glu
	275						280					285			
Ala	His	Gly	Leu	Lys	Pro	Val	Ile	Leu	Lys	Pro	Lys	Glu	Gly	Leu	Ala
	290					295					300				
Leu	Ile	Asn	Gly	Thr	Gln	Met	Ile	Thr	Ser	Leu	Gly	Cys	Glu	Ala	Val
305					310					315					320
Glu	Arg	Ala	Ser	Ala	Ile	Ala	Arg	Gln	Ala	Asp	Ile	Val	Ala	Ala	Leu
				325					330					335	
Thr	Leu	Glu	Val	Leu	Lys	Gly	Thr	Thr	Lys	Ala	Phe	Asp	Thr	Asp	Ile
			340					345					350		
His	Ala	Leu	Arg	Pro	His	Arg	Gly	Gln	Ile	Glu	Val	Ala	Phe	Arg	Phe
		355					360					365			
Arg	Ser	Leu	Leu	Asp	Ser	Leu	Arg	Cys	Cys	Pro	Gln	Val	His	Gly	Val
	370					375					380				
Val	Asn	Asp	Thr	Ile	Ala	Phe	Val	Lys	Asn	Ile	Ile	Thr	Thr	Glu	Leu
385					390					395					400
Asn	Ser	Ala	Thr	Asp	Asn	Pro	Met	Val	Phe	Ala	Asn	Arg	Gly	Glu	Thr
				405					410					415	
Val	Ser	Gly	Gly	Asn	Phe	His	Gly	Glu	Tyr	Pro	Ala	Lys	Ala	Leu	Asp
			420					425					430		
Tyr	Leu	Ala	Ile	Gly	Ile	His	Glu	Leu	Ala	Ala	Ile	Ser	Glu	Arg	Arg
		435					440					445			
Ile	Glu	Arg	Leu	Cys	Asn	Pro	Ser	Leu	Ser	Glu	Leu	Pro	Ala	Phe	Leu
	450					455					460				

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Val Ala Glu Gly Gly Leu Asn Ser Gly Phe Met Ile Ala His Cys Thr
 465 470 475 480

Ala Ala Ala Leu Val Ser Glu Asn Lys Ala Leu Cys His Pro Ser Ser
 485 490 495

Val Asp Ser Leu Ser Thr Ser Ala Ala Thr Glu Asp His Val Ser Met
 500 505 510

Gly Gly Trp Ala Ala Arg Lys Ala Leu Arg Val Ile Glu His Val Glu
 515 520 525

Gln Val Leu Ala Ile Glu Leu Leu Ala Ala Cys Gln Gly Ile Glu Phe
 530 535 540

Leu Arg Pro Leu Lys Thr Thr Thr Pro Leu Glu Lys Val Tyr Asp Leu
 545 550 555 560

Val Arg Ser Val Val Arg Pro Trp Ile Lys Asp Arg Phe Met Ala Pro
 565 570 575

Asp Ile Glu Ala Ala His Arg Leu Leu Leu Glu Gln Lys Val Trp Glu
 580 585 590

Val Ala Ala Pro Tyr Ile Glu Lys Tyr Arg Met Glu His Ile Pro Glu
 595 600 605

Ser Arg Pro Leu Ser Pro Thr Ala Phe Ser Leu Gln Phe Leu His Lys
 610 615 620

Lys Ser Thr Lys Ile Pro Glu Ser Glu Asp Leu
 625 630 635

<210> SEQ ID NO 39

<211> LENGTH: 677

<212> TYPE: PRT

<213> ORGANISM: Caenorhabditis elegans

<400> SEQUENCE: 39

Met Arg Leu Gln Val Gln Ile Gly Thr Glu Cys Val Val Val Pro Cys
 1 5 10 15

Lys Pro Asp Asp Thr Ile His Ala Val Ala Lys Lys Ser Val Glu Lys
 20 25 30

Leu Arg Arg Leu Arg Pro Lys Leu Pro Leu Ala Asp Asp Tyr Phe Glu
 35 40 45

Val Arg Arg Thr Val Gly Asn Ser Leu Leu Asp Pro Glu Asp Leu Val
 50 55 60

Ser Asp Val Leu Lys Asp Ser Asp Phe Ile Ile Val Ala Ala Ser Val
 65 70 75 80

Glu Glu Thr Glu Asp Ala Lys Glu Ala Lys Lys Gln Glu Glu Ile Asp
 85 90 95

Asn Ala Arg Ala Glu Ile Glu Lys Ile Asp Asn Arg Arg Arg Lys Val
 100 105 110

Ser Phe Ala Asp Ser Leu Ala Pro Met Val Leu Ala Pro Pro Thr Lys
 115 120 125

Leu Leu Ile Leu Asp Gly Asn Ser Leu Leu Pro Glu Asp Leu Val Arg
 130 135 140

Cys Glu Lys Gly Glu Cys Ala Ile Gln Leu Ser Met Glu Ser Glu Asp
 145 150 155 160

Arg Ile Arg Lys Ala Arg Thr Phe Leu Glu Lys Ile Ala Ser Glu His
 165 170 175

Arg Ala Val Tyr Gly Val Thr Thr Gly Phe Gly Thr Phe Ser Asn Val
 180 185 190

Thr Ile Pro Pro Glu Lys Leu Lys Lys Leu Gln Leu Asn Leu Ile Arg
 195 200 205

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Ser His Ala Thr Gly Tyr Gly Glu Pro Leu Ala Pro Asn Arg Ala Arg
 210 215 220

Met Leu Leu Ala Leu Arg Ile Asn Ile Leu Ala Lys Gly His Ser Gly
 225 230 235 240

Ile Ser Val Glu Asn Ile Lys Lys Met Ile Ala Ala Phe Asn Ala Phe
 245 250 255

Cys Val Ser Tyr Val Pro Gln Gln Gly Thr Val Gly Cys Ser Gly Asp
 260 265 270

Leu Cys Pro Leu Ala His Leu Ala Leu Gly Leu Leu Gly Glu Gly Lys
 275 280 285

Met Trp Ser Pro Thr Thr Gly Trp Gln Pro Ala Asp Val Val Leu Lys
 290 295 300

Lys Asn Asn Leu Glu Pro Leu Glu Leu Gly Pro Lys Glu Gly Leu Ala
 305 310 315 320

Leu Ile Asn Gly Thr Gln Met Val Thr Ala Leu Gly Ala Tyr Thr Leu
 325 330 335

Glu Arg Ala His Asn Ile Ala Arg Gln Ala Asp Val Ile Ala Ala Leu
 340 345 350

Ser Leu Asp Val Leu Lys Gly Thr Thr Arg Ala Tyr Asp Pro Asp Ile
 355 360 365

His Arg Ile Arg Pro His Arg Gly Gln Asn Leu Ser Ala Leu Arg Leu
 370 375 380

Arg Ala Leu Leu His Ser Glu Ala Asn Pro Ser Gln Ile Ala Glu Ser
 385 390 395 400

His Arg Asn Cys Thr Lys Val Gln Asp Ala Tyr Thr Leu Arg Cys Val
 405 410 415

Pro Gln Val His Gly Val Val His Asp Thr Ile Glu Phe Val Arg Glu
 420 425 430

Ile Ile Thr Thr Glu Met Asn Ser Ala Thr Asp Asn Pro Leu Val Phe
 435 440 445

Ala Asp Arg Glu Glu Ile Ile Ser Gly Gly Asn Phe His Gly Glu Tyr
 450 455 460

Pro Ala Lys Ala Leu Asp Phe Leu Ala Ile Ala Val Ala Glu Leu Ala
 465 470 475 480

Gln Met Ser Glu Arg Arg Leu Glu Arg Leu Val Asn Lys Glu Leu Ser
 485 490 495

Gly Leu Pro Thr Glu Leu Thr Pro Asp Gly Gly Leu Asn Ser Gly Phe
 500 505 510

Met Thr Val Gln Leu Cys Ala Ala Ser Leu Val Ser Glu Asn Lys Val
 515 520 525

Leu Cys His Pro Ser Ser Val Asp Ser Ile Pro Thr Ser Cys Asn Gln
 530 535 540

Glu Asp His Val Ser Met Gly Gly Phe Ala Ala Arg Lys Ala Leu Thr
 545 550 555 560

Val Val Glu His Val Glu Ala Val Leu Ala Met Glu Leu Leu Ala Ala
 565 570 575

Cys Gln Gly Ile Glu Phe Leu Lys Pro Leu Ile Ser Thr Ala Pro Leu
 580 585 590

His Lys Ile Tyr Gln Leu Val Arg Ser Val Ala Pro Pro Leu Asn Glu
 595 600 605

Asp Arg Tyr Met Lys Pro Glu Ile Asp Ala Val Leu Glu Met Ile Arg
 610 615 620

-continued

Glu Asn Arg Ile Trp Glu Ala Val Leu Pro His Leu Glu Thr Leu Glu
625 630 635 640

Ala Met Glu Glu Leu Asp Pro Asp Ala Leu Arg Gln Phe Thr Lys Thr
645 650 655

Pro Thr Gly Ile Val Gln Asp Arg Ser Met Ile Pro Ile Ser Asp Asp
660 665 670

Glu Glu Ser Ile Glu
675

<210> SEQ ID NO 40
<211> LENGTH: 508
<212> TYPE: PRT
<213> ORGANISM: Bacillus subtilis

<400> SEQUENCE: 40

Met Val Thr Leu Asp Gly Ser Ser Leu Thr Thr Ala Asp Val Ala Arg
1 5 10 15

Val Leu Phe Asp Phe Glu Glu Ala Ala Ser Glu Glu Ser Met Glu
20 25 30

Arg Val Lys Lys Ser Arg Ala Ala Val Glu Arg Ile Val Arg Asp Glu
35 40 45

Lys Thr Ile Tyr Gly Ile Asn Thr Gly Phe Gly Lys Phe Ser Asp Val
50 55 60

Leu Ile Gln Lys Glu Asp Ser Ala Ala Leu Gln Leu Asn Leu Ile Leu
65 70 75 80

Ser His Ala Cys Gly Val Gly Asp Pro Phe Pro Glu Cys Val Ser Arg
85 90 95

Ala Met Leu Leu Leu Arg Ala Asn Ala Leu Leu Lys Gly Phe Ser Gly
100 105 110

Val Arg Ala Glu Leu Ile Glu Gln Leu Leu Ala Phe Leu Asn Lys Arg
115 120 125

Val His Pro Val Ile Pro Gln Gln Gly Ser Leu Gly Ala Ser Gly Asp
130 135 140

Leu Ala Pro Leu Ser His Leu Ala Leu Ala Leu Ile Gly Gln Gly Glu
145 150 155 160

Val Phe Phe Glu Gly Glu Arg Met Pro Ala Met Thr Gly Leu Lys Lys
165 170 175

Ala Gly Ile Gln Pro Val Thr Leu Thr Ser Lys Glu Gly Leu Ala Leu
180 185 190

Ile Asn Gly Thr Gln Ala Met Thr Ala Met Gly Val Val Ala Tyr Ile
195 200 205

Glu Ala Glu Lys Leu Ala Tyr Gln Thr Glu Arg Ile Ala Ser Leu Thr
210 215 220

Ile Glu Gly Leu Gln Gly Ile Ile Asp Ala Phe Asp Glu Asp Ile His
225 230 235 240

Leu Ala Arg Gly Tyr Gln Glu Gln Ile Asp Val Ala Glu Arg Ile Arg
245 250 255

Phe Tyr Leu Ser Asp Ser Gly Leu Thr Thr Ser Gln Gly Glu Leu Arg
260 265 270

Val Gln Asp Ala Tyr Ser Leu Arg Cys Ile Pro Gln Val His Gly Ala
275 280 285

Thr Trp Gln Thr Leu Gly Tyr Val Lys Glu Lys Leu Glu Ile Glu Met
290 295 300

Asn Ala Ala Thr Asp Asn Pro Leu Ile Phe Asn Asp Gly Asp Lys Val
305 310 315 320

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Ile Ser Gly Gly Asn Phe His Gly Gln Pro Ile Ala Phe Ala Met Asp
 325 330 335

Phe Leu Lys Ile Ala Ile Ser Glu Leu Ala Asn Ile Ala Glu Arg Arg
 340 345 350

Ile Glu Arg Leu Val Asn Pro Gln Leu Asn Asp Leu Pro Pro Phe Leu
 355 360 365

Ser Pro His Pro Gly Leu Gln Ser Gly Ala Met Ile Met Gln Tyr Ala
 370 375 380

Ala Ala Ser Leu Val Ser Glu Asn Lys Thr Leu Ala His Pro Ala Ser
 385 390 395 400

Val Asp Ser Ile Pro Ser Ser Ala Asn Gln Glu Asp His Val Ser Met
 405 410 415

Gly Thr Ile Ala Ala Arg His Ala Tyr Gln Val Ile Ala Asn Thr Arg
 420 425 430

Arg Val Ile Ala Ile Glu Ala Ile Cys Ala Leu Gln Ala Val Glu Tyr
 435 440 445

Arg Gly Ile Glu His Ala Ala Ser Tyr Thr Lys Gln Leu Phe Gln Glu
 450 455 460

Met Arg Lys Val Val Pro Ser Ile Gln Gln Asp Arg Val Phe Ser Tyr
 465 470 475 480

Asp Ile Glu Arg Leu Thr Asp Trp Leu Lys Lys Glu Ser Leu Ile Pro
 485 490 495

Asp His Gln Asn Lys Glu Leu Arg Gly Met Asn Ile
 500 505

<210> SEQ ID NO 41

<211> LENGTH: 516

<212> TYPE: PRT

<213> ORGANISM: Streptomyces griseus

<400> SEQUENCE: 41

Met Asp Met His Thr Val Val Val Gly Thr Ser Gly Thr Thr Ala Glu
 1 5 10 15

Asp Val Val Ala Val Ala Arg His Gly Ala Arg Val Glu Leu Ser Ala
 20 25 30

Ala Ala Val Glu Ala Leu Ala Ala Ala Arg Leu Ile Val Asp Ala Leu
 35 40 45

Ala Ala Lys Pro Glu Pro Val Tyr Gly Val Ser Thr Gly Phe Gly Ala
 50 55 60

Leu Ala Ser Arg His Ile Gly Thr Glu Leu Arg Ala Gln Leu Gln Arg
 65 70 75 80

Asn Ile Val Arg Ser His Ala Ala Gly Met Gly Pro Arg Val Glu Arg
 85 90 95

Glu Val Val Arg Ala Leu Met Phe Leu Arg Leu Lys Thr Val Ala Ser
 100 105 110

Gly His Thr Gly Val Arg Pro Glu Val Ala Gln Thr Met Ala Asp Val
 115 120 125

Leu Asn Ala Gly Ile Thr Pro Val Val His Glu Tyr Gly Ser Leu Gly
 130 135 140

Cys Ser Gly Asp Leu Ala Pro Leu Ser His Cys Ala Leu Thr Leu Met
 145 150 155 160

Gly Glu Gly Glu Ala Glu Gly Pro Asp Gly Thr Val Arg Pro Ala Gly
 165 170 175

Glu Leu Leu Ala Ala His Gly Ile Ala Pro Val Glu Leu Arg Glu Lys

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180				185				190							
Glu	Gly	Leu	Ala	Leu	Leu	Asn	Gly	Thr	Asp	Gly	Met	Leu	Gly	Met	Leu
		195					200					205			
Val	Met	Ala	Leu	Ala	Asp	Leu	Arg	Asn	Leu	Tyr	Thr	Ser	Ala	Asp	Ile
	210					215					220				
Thr	Ala	Ala	Leu	Ser	Leu	Glu	Ala	Leu	Leu	Gly	Thr	Asp	Lys	Val	Leu
225					230					235					240
Ala	Pro	Glu	Leu	His	Ala	Ile	Arg	Pro	His	Pro	Gly	Gln	Gly	Val	Ser
				245					250					255	
Ala	Asp	Asn	Met	Ser	Arg	Val	Leu	Ala	Gly	Ser	Gly	Leu	Thr	Gly	His
			260					265				270			
His	Gln	Asp	Asp	Ala	Pro	Arg	Val	Gln	Asp	Ala	Tyr	Ser	Val	Arg	Cys
		275					280					285			
Ala	Pro	Gln	Val	Asn	Gly	Ala	Gly	Arg	Asp	Thr	Leu	Asp	His	Ala	Ala
		290				295					300				
Leu	Val	Ala	Gly	Arg	Glu	Leu	Ala	Ser	Ser	Val	Asp	Asn	Pro	Val	Val
305					310					315				320	
Leu	Pro	Asp	Gly	Arg	Val	Glu	Ser	Asn	Gly	Asn	Phe	His	Gly	Ala	Pro
				325					330					335	
Val	Ala	Tyr	Val	Leu	Asp	Phe	Leu	Ala	Ile	Val	Ala	Ala	Asp	Leu	Gly
			340						345				350		
Ser	Ile	Cys	Glu	Arg	Arg	Thr	Asp	Arg	Leu	Leu	Asp	Lys	Asn	Arg	Ser
		355					360					365			
His	Gly	Leu	Pro	Pro	Phe	Leu	Ala	Asp	Asp	Ala	Gly	Val	Asp	Ser	Gly
	370					375					380				
Leu	Met	Ile	Ala	Gln	Tyr	Thr	Gln	Ala	Ala	Leu	Val	Ser	Glu	Met	Lys
385					390					395					400
Arg	Leu	Ala	Val	Pro	Ala	Ser	Ala	Asp	Ser	Ile	Pro	Ser	Ser	Ala	Met
			405						410					415	
Gln	Glu	Asp	His	Val	Ser	Met	Gly	Trp	Ser	Ala	Ala	Arg	Lys	Leu	Arg
			420						425				430		
Thr	Ala	Val	Asp	Asn	Leu	Ala	Arg	Ile	Val	Ala	Val	Glu	Leu	Tyr	Ala
		435					440					445			
Ala	Thr	Arg	Ala	Ile	Glu	Leu	Arg	Ala	Ala	Glu	Gly	Leu	Thr	Pro	Ala
			450			455					460				
Pro	Ala	Ser	Glu	Ala	Val	Val	Ala	Ala	Leu	Arg	Ala	Ala	Gly	Ala	Glu
465					470					475					480
Gly	Pro	Gly	Pro	Asp	Arg	Phe	Leu	Ala	Pro	Asp	Leu	Ala	Ala	Ala	Asp
				485					490					495	
Thr	Phe	Val	Arg	Glu	Gly	Arg	Leu	Val	Ala	Ala	Val	Glu	Pro	Val	Thr
			500						505				510		
Gly	Pro	Leu	Ala												
		515													

<210> SEQ ID NO 42

<211> LENGTH: 511

<212> TYPE: PRT

<213> ORGANISM: Corynebacteriaceae sp.

<400> SEQUENCE: 42

Met	Ala	Ser	Ala	Pro	Gln	Ile	Thr	Leu	Gly	Leu	Ser	Gly	Ala	Thr	Ala
1				5					10					15	

Asp	Asp	Val	Ile	Ala	Val	Ala	Arg	His	Glu	Ala	Arg	Ile	Ser	Ile	Ser
		20						25					30		

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Pro Gln Val Leu Glu Glu Leu Ala Ser Val Arg Ala His Ile Asp Ala
 35 40 45
 Leu Ala Ser Ala Asp Thr Pro Val Tyr Gly Ile Ser Thr Gly Phe Gly
 50 55 60
 Ala Leu Ala Thr Arg His Ile Ala Pro Glu Asp Arg Ala Lys Leu Gln
 65 70 75 80
 Arg Ser Leu Ile Arg Ser His Ala Ala Gly Met Gly Glu Pro Val Glu
 85 90 95
 Arg Glu Val Val Arg Ala Leu Met Phe Leu Arg Ala Lys Thr Leu Ala
 100 105 110
 Ser Gly Arg Ser Val Arg Pro Val Val Leu Glu Thr Met Val Gly Met
 115 120 125
 Leu Asn Ala Gly Ile Thr Pro Val Val Arg Glu Tyr Gly Ser Leu Gly
 130 135 140
 Cys Ser Gly Asp Leu Ala Pro Leu Ser His Cys Ala Leu Val Leu Met
 145 150 155 160
 Gly Glu Gly Glu Ala Thr Asp Ala His Gly Asp Ile Arg Pro Val Pro
 165 170 175
 Glu Leu Phe Ala Glu Ala Gly Leu Thr Pro Val Glu Leu Ala Glu Lys
 180 185 190
 Glu Gly Leu Ala Leu Val Asn Gly Thr Asp Gly Met Leu Gly Gln Leu
 195 200 205
 Ile Met Ala Leu Ala Asp Leu Asp Glu Leu Leu Asp Ile Ala Asp Ala
 210 215 220
 Thr Ala Ala Met Ser Val Glu Ala Gln Leu Gly Thr Asp Gln Val Phe
 225 230 235 240
 Arg Ala Glu Leu His Glu Pro Leu Arg Pro His Pro Gly Gln Gly Arg
 245 250 255
 Ser Ala Gln Asn Met Phe Ala Phe Leu Ala Asp Ser Pro Ile Val Ala
 260 265 270
 Ser His Arg Glu Gly Asp Gly Arg Val Gln Asp Ala Tyr Ser Leu Arg
 275 280 285
 Cys Ser Pro Gln Val Thr Gly Ala Ala Arg Asp Thr Ile Ala His Ala
 290 295 300
 Arg Leu Val Ala Thr Arg Glu Leu Ala Ala Ala Ile Asp Asn Pro Val
 305 310 315 320
 Val Leu Pro Ser Gly Glu Val Thr Ser Asn Gly Asn Phe His Gly Ala
 325 330 335
 Pro Val Ala Tyr Val Leu Asp Phe Leu Ala Ile Ala Val Ala Asp Leu
 340 345 350
 Gly Ser Ile Ala Glu Arg Arg Thr Asp Arg Met Leu Asp Pro Ala Arg
 355 360 365
 Ser Arg Asp Leu Pro Ala Phe Leu Ala Asp Asp Pro Gly Val Asp Ser
 370 375 380
 Gly Met Met Ile Ala Gln Tyr Thr Gln Ala Gly Leu Val Ala Glu Asn
 385 390 395 400
 Lys Arg Leu Ala Val Pro Ala Val Asp Ser Ile Pro Ser Ser Ala Met
 405 410 415
 Gln Glu Asp His Val Ser Leu Gly Trp His Ala Ala Arg Lys Leu Pro
 420 425 430
 Thr Ser Val Ala Asn Leu Arg Arg Ile Leu Ala Val Glu Met Leu Ile
 435 440 445
 Ala Gly Arg Ala Leu Asp Leu Arg Ala Pro Leu Lys Pro Gly Pro Ala

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      450              455              460
Thr Gly Ala Val Leu Glu Val Leu Arg Ser Lys Val Ala Gly Pro Gly
465              470              475              480

Gln Asp Arg Phe Leu Ser Ala Glu Leu Glu Ala Ala Tyr Asp Leu Leu
              485              490              495

Ala Asn Gly Ser Val His Lys Ala Leu Glu Ala His Leu Pro Glu
              500              505              510

<210> SEQ ID NO 43
<211> LENGTH: 513
<212> TYPE: PRT
<213> ORGANISM: Unknown Organism
<220> FEATURE:
<223> OTHER INFORMATION: Description of Unknown Organism: 983831/HAL

<400> SEQUENCE: 43

Met Ala Ser Ala Pro Gln Ile Thr Leu Gly Leu Ser Gly Ala Thr Ala
 1              5              10              15

Asp Asp Val Ile Ala Val Ala Arg His Glu Ala Arg Ile Ser Ile Ser
              20              25              30

Pro Gln Val Leu Glu Glu Leu Ala Ser Val Arg Ala His Ile Asp Ala
              35              40              45

Leu Ala Ser Ala Asp Thr Pro Val Tyr Gly Ile Ser Thr Gly Phe Gly
 50              55              60

Ala Leu Ala Thr Arg His Ile Ala Pro Glu Asp Arg Ala Lys Leu Gln
 65              70              75              80

Arg Ser Leu Ile Arg Ser His Ala Ala Gly Met Gly Glu Pro Val Glu
              85              90              95

Arg Glu Val Val Arg Ala Leu Met Phe Leu Arg Ala Lys Thr Leu Ala
              100             105             110

Ser Gly Arg Thr Gly Val Arg Pro Val Val Leu Glu Thr Met Val Gly
              115             120             125

Met Leu Asn Ala Gly Ile Thr Pro Val Val Arg Glu Tyr Gly Ser Leu
              130             135             140

Gly Cys Ser Gly Asp Leu Ala Pro Leu Ser His Cys Ala Leu Val Leu
              145             150             155             160

Met Gly Glu Gly Glu Ala Thr Asp Ala His Gly Asp Ile Arg Pro Val
              165             170             175

Pro Glu Leu Phe Ala Glu Ala Gly Leu Thr Pro Val Glu Leu Ala Glu
              180             185             190

Lys Glu Gly Leu Ala Leu Val Asn Gly Thr Asp Gly Met Leu Gly Gln
              195             200             205

Leu Ile Met Ala Leu Ala Asp Leu Asp Glu Leu Leu Asp Ile Ala Asp
              210             215             220

Ala Thr Ala Ala Met Ser Val Glu Ala Gln Leu Gly Thr Asp Gln Val
              225             230             235             240

Phe Arg Ala Glu Leu His Glu Pro Leu Arg Pro His Pro Gly Gln Gly
              245             250             255

Arg Ser Ala Gln Asn Met Phe Ala Phe Leu Ala Asp Ser Pro Ile Val
              260             265             270

Ala Ser His Arg Glu Gly Asp Gly Arg Val Gln Asp Ala Tyr Ser Leu
              275             280             285

Arg Cys Ser Pro Gln Val Thr Gly Ala Ala Arg Asp Thr Ile Ala His
              290             295             300

Ala Arg Leu Val Ala Thr Arg Glu Leu Ala Ala Ala Ile Asp Asn Pro

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305	310	315	320
Val Val Leu Pro Ser Gly Glu Val Thr Ser Asn Gly Asn Phe His Gly			
	325	330	335
Ala Pro Val Ala Tyr Val Leu Asp Phe Leu Ala Ile Ala Val Ala Asp			
	340	345	350
Leu Gly Ser Ile Ala Glu Arg Arg Thr Asp Arg Met Leu Asp Pro Ala			
	355	360	365
Arg Ser Arg Asp Leu Pro Ala Phe Leu Ala Asp Asp Pro Gly Val Asp			
	370	375	380
Ser Gly Met Met Ile Ala Gln Tyr Thr Gln Ala Gly Leu Val Ala Glu			
	385	390	395
Asn Lys Arg Leu Ala Val Pro Ala Ser Val Asp Ser Ile Pro Ser Ser			
	405	410	415
Ala Met Gln Glu Asp His Val Ser Leu Gly Trp His Ala Ala Arg Lys			
	420	425	430
Leu Arg Thr Ser Val Ala Asn Leu Arg Arg Ile Leu Ala Val Glu Met			
	435	440	445
Leu Ile Ala Gly Arg Ala Leu Asp Leu Arg Ala Pro Leu Lys Pro Gly			
	450	455	460
Pro Ala Thr Gly Ala Val Leu Glu Val Leu Arg Ser Lys Val Ala Gly			
	465	470	475
Pro Gly Gln Asp Arg Phe Leu Ser Ala Glu Leu Glu Ala Ala Tyr Asp			
	485	490	495
Leu Leu Ala Asn Gly Ser Val His Lys Ala Leu Glu Ala His Leu Pro			
	500	505	510

Ala

<210> SEQ ID NO 44
 <211> LENGTH: 513
 <212> TYPE: PRT
 <213> ORGANISM: Streptomyces coelicolor

<400> SEQUENCE: 44

Met Ala Ser Met His Thr Val Val Val Gly Thr Ser Gly Val Thr Ala			
1	5	10	15
Ser Asp Val Leu Ala Val Ala Arg Ala Gly Ala Arg Ile Glu Leu Ser			
	20	25	30
Glu Glu Ala Val Ala Ala Leu Ala Ala Arg Ser Val Val Asp Ala			
	35	40	45
Leu Ala Ala Lys Pro Asp Pro Val Tyr Gly Val Ser Thr Gly Phe Gly			
	50	55	60
Ala Leu Ala Thr Arg His Ile Ser Pro Glu Leu Arg Gly Arg Leu Gln			
	65	70	75
Arg Asn Ile Val Arg Ser His Ala Ala Gly Met Gly Pro Arg Val Glu			
	85	90	95
Arg Glu Val Val Arg Ala Leu Met Phe Leu Arg Leu Lys Thr Val Cys			
	100	105	110
Ser Gly Arg Thr Gly Val Arg Pro Glu Val Ala Gln Thr Met Ala Asp			
	115	120	125
Val Leu Asn Ala Gly Ile Thr Pro Val Val His Glu Tyr Gly Ser Leu			
	130	135	140
Gly Cys Ser Gly Asp Leu Ala Pro Leu Ser His Cys Ala Leu Thr Leu			
	145	150	155
Met Gly Glu Gly Asp Ala Glu Gly Pro Asp Gly Thr Val Arg Pro Ala			

-continued

165					170					175					
Gly	Glu	Leu	Leu	Ala	Ala	His	Gly	Ile	Ala	Pro	Val	Glu	Leu	Arg	Glu
			180					185					190		
Lys	Glu	Gly	Leu	Ala	Leu	Leu	Asn	Gly	Thr	Asp	Gly	Met	Leu	Gly	Met
		195					200					205			
Leu	Val	Met	Ala	Leu	Ala	Asp	Leu	Asp	Thr	Leu	Tyr	Lys	Ser	Ala	Asp
		210				215					220				
Ile	Thr	Ala	Ala	Leu	Thr	Met	Glu	Ala	Leu	Leu	Gly	Thr	Asp	Arg	Val
225					230					235					240
Leu	Ala	Pro	Glu	Leu	His	Ala	Pro	Ile	Arg	Pro	His	Pro	Gly	Gln	Ala
				245					250					255	
Ala	Ser	Ala	Ala	Asn	Met	Ala	Ala	Val	Leu	Lys	Gly	Ser	Gly	Leu	Thr
			260					265					270		
Gly	His	His	Gln	Asp	Asp	Ala	Pro	Arg	Val	Gln	Asp	Ala	Tyr	Ser	Val
		275					280					285			
Arg	Cys	Ala	Pro	Gln	Val	Ala	Gly	Ala	Gly	Arg	Asp	Thr	Met	Ala	His
	290					295					300				
Ala	Gly	Leu	Val	Ala	Glu	Arg	Glu	Leu	Ala	Ala	Ala	Val	Asp	Asn	Pro
305					310					315				320	
Val	Val	Leu	Pro	Asp	Gly	Arg	Val	Glu	Ser	Asn	Gly	Asn	Phe	His	Gly
				325					330					335	
Ala	Pro	Val	Ala	Tyr	Val	Leu	Asp	Phe	Leu	Ala	Val	Ala	Val	Ala	Asp
			340					345					350		
Leu	Gly	Ser	Ile	Ala	Glu	Arg	Arg	Thr	Asp	Arg	Leu	Leu	Asp	Lys	Asn
		355					360					365			
Arg	Ser	His	Gly	Leu	Pro	Pro	Phe	Leu	Ala	Asp	Asp	Ala	Gly	Val	Asp
		370					375					380			
Ser	Gly	Leu	Met	Ile	Ala	Gln	Tyr	Thr	Gln	Ala	Ala	Leu	Val	Gly	Glu
385					390					395					400
Leu	Lys	Arg	Leu	Ala	Val	Pro	Ala	Ser	Ala	Asp	Ser	Ile	Pro	Ser	Ser
				405					410					415	
Ala	Met	Gln	Glu	Asp	His	Val	Ser	Met	Gly	Trp	Ser	Ala	Ala	Arg	Lys
			420					425					430		
Leu	Arg	Thr	Ala	Val	Asp	Asn	Leu	Ala	Arg	Val	Ile	Ala	Val	Glu	Leu
		435					440					445			
Tyr	Ala	Ala	Thr	Arg	Ala	Ile	Gln	Leu	Arg	Glu	Gly	Leu	Thr	Pro	Ala
		450				455					460				
Pro	Ala	Ser	Gln	Ala	Val	Val	Glu	Ala	Val	Arg	Ala	Ala	Val	Glu	Gly
465					470					475				480	
Pro	Gly	Pro	Asp	Arg	His	Leu	Ala	Pro	Asp	Leu	Ala	Ala	Ala	Asp	Ala
				485					490					495	
Phe	Val	Arg	Ala	Gly	His	Leu	Val	Ala	Ala	Ala	Glu	Ser	Val	Thr	Gly
			500					505					510		

Pro

<210> SEQ ID NO 45

<211> LENGTH: 513

<212> TYPE: PRT

<213> ORGANISM: Streptomyces griseus

<400> SEQUENCE: 45

Met	Met	Asp	Met	His	Thr	Val	Val	Val	Gly	Thr	Ser	Gly	Thr	Thr	Ala
1				5					10					15	

Glu Asp Val Val Ala Val Ala Arg His Gly Ala Arg Val Glu Leu Ser

-continued

20					25					30					
Ala	Ala	Ala	Val	Glu	Ala	Leu	Ala	Ala	Ala	Arg	Leu	Ile	Val	Asp	Ala
		35					40					45			
Leu	Ala	Ala	Lys	Pro	Glu	Pro	Val	Tyr	Gly	Val	Ser	Thr	Gly	Phe	Gly
	50					55					60				
Ala	Leu	Ala	Ser	Arg	His	Ile	Gly	Thr	Glu	Leu	Arg	Ala	Gln	Leu	Gln
65					70					75					80
Arg	Asn	Ile	Val	Arg	Ser	His	Ala	Ala	Gly	Met	Gly	Pro	Arg	Val	Glu
				85					90					95	
Arg	Glu	Val	Val	Arg	Ala	Leu	Met	Phe	Leu	Arg	Leu	Lys	Thr	Val	Ala
			100					105						110	
Ser	Gly	His	Thr	Gly	Val	Arg	Pro	Glu	Val	Ala	Gln	Thr	Met	Ala	Asp
		115					120					125			
Val	Leu	Asn	Ala	Gly	Ile	Thr	Pro	Val	Val	His	Glu	Tyr	Gly	Ser	Leu
	130					135					140				
Gly	Cys	Ser	Gly	Asp	Leu	Ala	Pro	Leu	Ser	His	Cys	Ala	Leu	Thr	Leu
145					150					155					160
Met	Gly	Glu	Gly	Glu	Ala	Glu	Gly	Pro	Asp	Gly	Thr	Val	Arg	Pro	Ala
				165					170					175	
Gly	Glu	Leu	Leu	Ala	Ala	His	Gly	Ile	Ala	Pro	Val	Glu	Leu	Arg	Glu
			180					185						190	
Lys	Glu	Gly	Leu	Ala	Leu	Leu	Asn	Gly	Thr	Asp	Gly	Met	Leu	Gly	Met
		195					200					205			
Leu	Val	Met	Ala	Leu	Ala	Asp	Leu	Arg	Asn	Leu	Tyr	Thr	Ser	Ala	Asp
	210					215					220				
Ile	Thr	Ala	Ala	Leu	Ser	Leu	Glu	Ala	Leu	Leu	Gly	Thr	Asp	Lys	Val
225						230					235				240
Leu	Ala	Pro	Glu	Leu	His	Ala	Pro	Ile	Arg	Pro	His	Pro	Gly	Gln	Gly
				245					250					255	
Val	Ser	Ala	Asp	Asn	Met	Ser	Arg	Val	Leu	Ala	Gly	Ser	Gly	Leu	Thr
			260					265						270	
Gly	His	His	Gln	Asp	Asp	Ala	Pro	Arg	Val	Gln	Asp	Ala	Tyr	Ser	Val
		275					280					285			
Arg	Cys	Ala	Pro	Gln	Val	Asn	Gly	Ala	Gly	Arg	Asp	Thr	Leu	Asp	His
	290					295					300				
Ala	Ala	Leu	Val	Ala	Gly	Arg	Glu	Leu	Ala	Ser	Ser	Val	Asp	Asn	Pro
305					310						315				320
Val	Val	Leu	Pro	Asp	Gly	Arg	Val	Glu	Ser	Asn	Gly	Asn	Phe	His	Gly
				325					330					335	
Ala	Pro	Val	Ala	Tyr	Val	Leu	Asp	Phe	Leu	Ala	Ile	Val	Ala	Ala	Asp
			340					345						350	
Leu	Gly	Ser	Ile	Cys	Glu	Arg	Arg	Thr	Asp	Arg	Leu	Leu	Asp	Lys	Asn
		355					360					365			
Arg	Ser	His	Gly	Leu	Pro	Pro	Phe	Leu	Ala	Asp	Asp	Ala	Gly	Val	Asp
		370					375					380			
Ser	Gly	Leu	Met	Ile	Ala	Gln	Tyr	Thr	Gln	Ala	Ala	Leu	Val	Ser	Glu
385						390					395				400
Met	Lys	Arg	Leu	Ala	Val	Pro	Ala	Ser	Ala	Asp	Ser	Ile	Pro	Ser	Ser
				405					410					415	
Ala	Met	Gln	Glu	Asp	His	Val	Ser	Met	Gly	Trp	Ser	Ala	Ala	Arg	Lys
			420					425						430	
Leu	Arg	Thr	Ala	Val	Asp	Asn	Leu	Ala	Arg	Ile	Val	Ala	Val	Glu	Leu
		435					440					445			

-continued

Tyr Ala Ala Thr Arg Ala Ile Glu Leu Arg Ala Ala Leu Thr Pro Ala
 450 455 460
 Pro Ala Ser Glu Ala Val Val Ala Ala Leu Arg Ala Ala Gly Ala Gly
 465 470 475 480
 Pro Gly Pro Asp Arg Phe Leu Ala Pro Asp Leu Ala Ala Ala Asp Thr
 485 490 495
 Phe Val Arg Glu Gly Arg Leu Val Ala Ala Val Glu Pro Val Thr Gly
 500 505 510
 Pro

<210> SEQ ID NO 46
 <211> LENGTH: 513
 <212> TYPE: PRT
 <213> ORGANISM: Deinococcus radiodurans

<400> SEQUENCE: 46

Met Ala Ser Ala Pro Gln Ile Met Ile Leu Asp Arg Asp Leu Asn Leu
 1 5 10 15
 Glu Gln Phe Ile Ser Val Val Arg His Gly Glu Gln Val Glu Leu Ser
 20 25 30
 Ala Ala Ala Arg Glu Arg Ile Ala Arg Ala Arg Thr Val Ile Glu Gln
 35 40 45
 Ile Val Glu Gly Asp Thr Pro Ile Tyr Gly Val Asn Thr Gly Phe Gly
 50 55 60
 Lys Phe Glu Asn Val Gln Ile Asp Arg Ser Gln Leu Ala Gln Leu Gln
 65 70 75 80
 His Asn Leu Ile Val Ser His Ala Ile Gly Met Gly Glu Pro Leu Pro
 85 90 95
 Ala Glu Val Val Arg Gly Met Leu Leu Leu Arg Ala Gln Ser Leu Ser
 100 105 110
 Leu Gly His Ser Gly Val Arg Val Glu Val Val Glu Leu Leu Leu Ala
 115 120 125
 Leu Leu Asn Ala Asp Ala Leu Pro Val Val Pro Ser Gln Gly Ser Val
 130 135 140
 Gly Ala Ser Gly Asp Leu Ala Pro Leu Ala His Leu Ala Leu Gly Leu
 145 150 155 160
 Ile Gly Leu Gly Asp Ile Thr Glu Tyr Gln Gly Gln Val Arg Pro Ala
 165 170 175
 Ala Asp Val Leu Ala Glu Leu Gly Leu Ser Pro Val Gln Leu Gln Ala
 180 185 190
 Lys Glu Gly Leu Ala Leu Ile Asn Gly Thr Gln Leu Met Gly Ser Leu
 195 200 205
 Leu Ala Leu Ala Leu His Asp Ala Gln Val Leu Leu Gly Thr Ala Asn
 210 215 220
 Leu Ala Ala Ala Met Thr Val Glu Ala Arg Tyr Gly Ser His Arg Pro
 225 230 235 240
 Phe Gln Pro Asp Val His Val Gly Leu Arg Pro His Pro Gly Ala Leu
 245 250 255
 Ala Val Ala Ala Glu Leu Arg Glu Phe Leu Ala Gly Ser Glu Ile Ala
 260 265 270
 Pro Ser His Leu Thr Gly Asp Gly Lys Val Gln Asp Ala Tyr Ser Leu
 275 280 285
 Arg Ala Val Pro Gln Val His Gly Ala Thr Trp Asp Ala Leu Ala Gln
 290 295 300

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Ala Glu Arg Val Leu Ala Val Glu Phe Ala Ser Val Thr Asp Asn Pro
 305 310 315 320

Leu Ile Phe Pro Thr Gly Glu Val Val Ser Gly Gly Asn Phe His Gly
 325 330 335

Gln Pro Leu Ala Val Thr Ile Asp Ala Leu Lys Val Ala Val Ala Glu
 340 345 350

Leu Gly Ser Ile Ser Glu Arg Arg Thr Glu Gln Leu Leu Asn Pro Ala
 355 360 365

Leu Ser Arg Gly Leu Pro Ala Phe Leu Thr Pro Asn Gly Gly Leu Asn
 370 375 380

Ser Gly Phe Met Ile Ala Gln Tyr Thr Ser Ala Ala Leu Val Ser Glu
 385 390 395 400

Asn Lys Val Leu Ser His Pro Ala Ser Val Asp Ser Ile Pro Thr Ser
 405 410 415

Ala Asn Gln Glu Asp His Val Ser Met Gly Ala His Ala Ala Arg Gln
 420 425 430

Leu Arg Gln Ile Val Ala Asn Val Gln Thr Val Leu Ser Ile Glu Leu
 435 440 445

Leu Cys Ala Ala Gln Gly Leu Asp Phe Gln Gln Pro Leu Arg Ala Gly
 450 455 460

Arg Gly Val Gln Ala Ala Tyr Glu Tyr Val Arg Thr Phe Val Pro Thr
 465 470 475 480

Leu Thr Glu Asp Arg Tyr Phe Arg Pro Asp Leu Leu Arg Leu Arg Gly
 485 490 495

Glu Leu Val Ser Gly Arg Val Ala Gln Ala Ala Asp Thr Gln Ala Pro
 500 505 510

Ala

<210> SEQ ID NO 47

<211> LENGTH: 513

<212> TYPE: PRT

<213> ORGANISM: Agrobacterium rhizogenes

<400> SEQUENCE: 47

Met Ala Ser Ala Pro Gln Ile Thr Leu Gly Leu Ser Gly Val Pro Leu
 1 5 10 15

His His Leu Ala Asp Ile Tyr Trp Asn Asn Gly Ser Ala Lys Leu Asp
 20 25 30

Pro Ser Phe Asp Ala Ala Val Leu Lys Gly Ala Ala Arg Ile Ala Glu
 35 40 45

Ile Ala Ala Gly Asn Ala Pro Val Tyr Gly Ile Asn Thr Gly Phe Gly
 50 55 60

Lys Leu Ala Ser Ile Lys Ile Asp Ala Ala Asp Leu Ala Thr Leu Gln
 65 70 75 80

Arg Asn Leu Ile Leu Ser His Cys Cys Gly Val Gly Ala Pro Leu Pro
 85 90 95

Glu Asn Val Val Arg Leu Ile Met Ala Leu Lys Leu Ile Ser Leu Gly
 100 105 110

Arg Gly Ala Ser Gly Val Arg Ile Glu Leu Ile Arg Leu Ile Glu Gly
 115 120 125

Met Leu Glu Lys Gly Val Ile Pro Val Ile Pro Glu Lys Gly Ser Val
 130 135 140

Gly Ala Ser Gly Asp Leu Ala Pro Leu Ala His Met Ser Ala Thr Met
 145 150 155 160

-continued

Met Gly Glu Gly Glu Ala Phe Asp Tyr Gln Gly Val Gln Met Pro Ser
 165 170 175
 Lys Asp Ala Leu Ala Lys Ala Gly Leu Ser Pro Val Val Leu Ala Ala
 180 185 190
 Lys Glu Gly Leu Ala Leu Ile Asn Gly Thr Gln Thr Ser Thr Ala Leu
 195 200 205
 Ala Leu Ala Gly Leu Phe Arg Ala His Arg Ala Ala Gln Ser Ala Leu
 210 215 220
 Val Thr Gly Ala Leu Ser Thr Asp Ala Ala Met Gly Ser Ser Ala Pro
 225 230 235 240
 Phe His Pro Asp Ile His Thr Pro Leu Arg Gly His Lys Gly Gln Ile
 245 250 255
 Asp Ala Gly Ser Ala Leu Arg Asn Leu Leu Gln Gly Ser Glu Ile Arg
 260 265 270
 Glu Ser His Ile Glu Gly Asp Glu Arg Val Gln Asp Pro Tyr Cys Ile
 275 280 285
 Arg Cys Gln Pro Gln Val Asp Gly Ala Cys Leu Asp Leu Leu Ala Ser
 290 295 300
 Val Ala Arg Thr Leu Glu Ile Glu Ala Asn Ala Val Thr Asp Asn Pro
 305 310 315 320
 Leu Val Leu Ser Asp Asn Ser Val Val Ser Gly Gly Asn Phe His Ala
 325 330 335
 Glu Pro Val Ala Phe Ala Ala Asp Gln Thr Ala Leu Ala Val Cys Glu
 340 345 350
 Ile Gly Ala Ile Ala Gln Arg Arg Ile Ala Leu Leu Val Asp Pro Ala
 355 360 365
 Leu Ser Tyr Gly Leu Pro Ala Phe Leu Ser Lys Lys Pro Gly Leu Asn
 370 375 380
 Ser Gly Leu Met Ile Ala Glu Val Thr Ser Ala Ala Leu Met Ser Glu
 385 390 395 400
 Asn Lys Gln Met Ser His Pro Ala Ser Val Asp Ser Thr Pro Thr Ser
 405 410 415
 Ala Asn Gln Glu Asp His Val Ser Met Ala Cys His Gly Ala Arg Arg
 420 425 430
 Leu Leu Ala Met Thr Asp Asn Leu Phe Gly Ile Leu Gly Ile Glu Ala
 435 440 445
 Leu Ala Ala Val Gln Gly Val Glu Leu Arg Gly Pro Leu Lys Thr Ser
 450 455 460
 Pro Glu Leu Glu Lys Ala Ala Ala Val Leu Arg Ser Ala Val Pro Val
 465 470 475 480
 Leu Glu Asp Asp Arg Tyr Met Ala Thr Asp Leu Lys Ala Ala Ile Glu
 485 490 495
 Val Val Ala Ser Gly Ala Leu Val Ser Ala Ile Ser Ser Gly Leu Pro
 500 505 510
 Val

<210> SEQ ID NO 48

<211> LENGTH: 513

<212> TYPE: PRT

<213> ORGANISM: Agrobacterium rhizogenes

<400> SEQUENCE: 48

Met Ala Ser Ala Pro Gln Ile Thr Leu Gly Leu Ser Gly Val Pro Leu
 1 5 10 15

-continued

His His Leu Ala Asp Ile Tyr Trp Asn Asn Gly Ser Ala Lys Leu Asp
 20 25 30
 Pro Ser Phe Asp Ala Ala Val Leu Lys Gly Ala Ala Arg Ile Ala Glu
 35 40 45
 Ile Ala Ala Gly Asn Ala Pro Val Tyr Gly Ile Asn Thr Gly Phe Gly
 50 55 60
 Lys Leu Ala Ser Ile Lys Ile Asp Ala Ala Asp Leu Ala Thr Leu Gln
 65 70 75 80
 Arg Asn Leu Ile Leu Ser His Cys Cys Gly Val Gly Ala Pro Leu Pro
 85 90 95
 Glu Asn Val Val Arg Leu Ile Met Ala Leu Lys Leu Ile Ser Leu Gly
 100 105 110
 Arg Gly Ala Ser Gly Val Arg Ile Glu Leu Ile Arg Leu Ile Glu Gly
 115 120 125
 Met Leu Glu Lys Gly Val Ile Pro Val Ile Pro Glu Lys Gly Ser Val
 130 135 140
 Gly Ala Ser Gly Asp Leu Ala Pro Leu Ala His Met Ser Ala Thr Met
 145 150 155 160
 Met Gly Glu Gly Glu Ala Phe Asp Tyr Gln Gly Val Gln Met Pro Ser
 165 170 175
 Lys Asp Ala Leu Ala Lys Ala Gly Leu Ser Pro Val Val Leu Ala Ala
 180 185 190
 Lys Glu Gly Leu Ala Leu Ile Asn Gly Thr Gln Thr Ser Thr Ala Leu
 195 200 205
 Ala Leu Ala Gly Leu Phe Arg Ala His Arg Ala Ala Gln Ser Ala Leu
 210 215 220
 Val Thr Gly Ala Leu Ser Thr Asp Ala Ala Met Gly Ser Ser Ala Pro
 225 230 235 240
 Phe His Pro Asp Ile His Thr Pro Leu Arg Gly His Lys Gly Gln Ile
 245 250 255
 Asp Ala Gly Ser Ala Leu Arg Asn Leu Leu Gln Gly Ser Glu Ile Arg
 260 265 270
 Glu Ser His Ile Glu Gly Asp Glu Arg Val Gln Asp Pro Tyr Cys Ile
 275 280 285
 Arg Cys Gln Pro Gln Val Asp Gly Ala Cys Leu Asp Leu Leu Ala Ser
 290 295 300
 Val Ala Arg Thr Leu Glu Ile Glu Ala Asn Ala Val Thr Asp Asn Pro
 305 310 315 320
 Leu Val Leu Ser Asp Asn Ser Val Val Ser Gly Gly Asn Phe His Ala
 325 330 335
 Glu Pro Val Ala Phe Ala Ala Asp Gln Thr Ala Leu Ala Val Cys Glu
 340 345 350
 Ile Gly Ala Ile Ala Gln Arg Arg Ile Ala Leu Leu Val Asp Pro Ala
 355 360 365
 Leu Ser Tyr Gly Leu Pro Ala Phe Leu Ser Lys Lys Pro Gly Leu Asn
 370 375 380
 Ser Gly Leu Met Ile Ala Glu Val Thr Ser Ala Ala Leu Met Ser Glu
 385 390 395 400
 Asn Lys Gln Met Ser His Pro Ala Ser Val Asp Ser Thr Pro Thr Ser
 405 410 415
 Ala Asn Gln Glu Asp His Val Ser Met Ala Cys His Gly Ala Arg Arg
 420 425 430

-continued

Leu Leu Ala Met Thr Asp Asn Leu Phe Gly Ile Leu Gly Ile Glu Ala
 435 440 445

Leu Ala Ala Val Gln Gly Val Glu Leu Arg Gly Pro Leu Lys Thr Ser
 450 455 460

Pro Glu Leu Glu Lys Ala Ala Ala Val Leu Arg Ser Ala Val Pro Val
 465 470 475 480

Leu Glu Asp Asp Arg Tyr Met Ala Thr Asp Leu Lys Ala Ala Ile Glu
 485 490 495

Val Val Ala Ser Gly Ala Leu Val Ser Ala Ile Ser Ser Gly Leu Pro
 500 505 510

Val

<210> SEQ ID NO 49
 <211> LENGTH: 513
 <212> TYPE: PRT
 <213> ORGANISM: Bacillus subtilis

<400> SEQUENCE: 49

Met Ala Ser Ala Pro Met Val Thr Leu Asp Gly Ser Ser Leu Thr Thr
 1 5 10 15

Ala Asp Val Ala Arg Val Leu Phe Asp Phe Glu Glu Ala Ala Ala Ser
 20 25 30

Glu Glu Ser Met Glu Arg Val Lys Lys Ser Arg Ala Ala Val Glu Arg
 35 40 45

Ile Val Arg Asp Glu Lys Thr Ile Tyr Gly Ile Asn Thr Gly Phe Gly
 50 55 60

Lys Phe Ser Asp Val Leu Ile Gln Lys Glu Asp Ser Ala Ala Leu Gln
 65 70 75 80

Leu Asn Leu Ile Leu Ser His Ala Cys Gly Val Gly Asp Pro Phe Pro
 85 90 95

Glu Cys Val Ser Arg Ala Met Leu Leu Leu Arg Ala Asn Ala Leu Leu
 100 105 110

Lys Gly Phe Ser Gly Val Arg Ala Glu Leu Ile Glu Gln Leu Leu Ala
 115 120 125

Phe Leu Asn Lys Arg Val His Pro Val Ile Pro Gln Gln Gly Ser Leu
 130 135 140

Gly Ala Ser Gly Asp Leu Ala Pro Leu Ser His Leu Ala Leu Ala Leu
 145 150 155 160

Ile Gly Gln Gly Glu Val Phe Asp Phe Glu Gly Glu Arg Met Pro Ala
 165 170 175

Met Thr Gly Leu Lys Lys Ala Gly Ile Gln Pro Val Thr Leu Thr Ser
 180 185 190

Lys Glu Gly Leu Ala Leu Ile Asn Gly Thr Gln Ala Met Thr Ala Met
 195 200 205

Gly Val Val Ala Tyr Ile Glu Ala Glu Lys Leu Ala Tyr Gln Thr Glu
 210 215 220

Arg Ile Ala Ser Leu Thr Ile Glu Gly Leu Gln Gly Ile Ile Asp Ala
 225 230 235 240

Phe Asp Glu Asp Ile His Leu Ala Leu Arg Gly Tyr Gln Glu Gln Ile
 245 250 255

Asp Val Ala Glu Arg Ile Arg Phe Tyr Leu Ser Asp Ser Gly Leu Thr
 260 265 270

Thr Ser His Arg Gln Gly Glu Leu Arg Val Gln Asp Ala Tyr Ser Leu
 275 280 285

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Arg Cys Ile Pro Gln Val His Gly Ala Thr Trp Gln Thr Leu Gly Tyr
 290 295 300
 Val Lys Glu Lys Leu Glu Ile Glu Met Asn Ala Ala Thr Asp Asn Pro
 305 310 315 320
 Leu Ile Phe Asn Asp Gly Asp Val Ile Ser Gly Gly Asn Phe His Gly
 325 330 335
 Gln Pro Ile Ala Phe Ala Met Asp Phe Leu Lys Ile Ala Ile Ser Glu
 340 345 350
 Leu Ala Asn Ile Ala Glu Arg Arg Ile Glu Arg Leu Val Asn Pro Gln
 355 360 365
 Leu Asn Arg Asp Leu Pro Pro Phe Leu Ser Pro His Pro Gly Leu Gln
 370 375 380
 Ser Gly Ala Met Ile Met Gln Tyr Ala Ala Ala Ser Leu Val Ser Glu
 385 390 395 400
 Asn Lys Thr Leu Ala His Pro Ala Ser Val Asp Ser Ile Pro Ser Ser
 405 410 415
 Ala Asn Gln Glu Asp His Val Ser Met Gly Thr Ile Ala Ala Arg His
 420 425 430
 Ala Tyr Gln Val Ile Ala Asn Thr Arg Arg Val Ile Ala Ile Glu Ala
 435 440 445
 Ile Cys Ala Leu Gln Ala Val Glu Tyr Arg Gly Ile Glu His Ala Ala
 450 455 460
 Ser Tyr Thr Lys Gln Leu Phe Gln Glu Met Arg Lys Val Val Pro Ser
 465 470 475 480
 Ile Gln Gln Asp Arg Val Phe Ser Tyr Asp Ile Glu Arg Leu Thr Asp
 485 490 495
 Trp Leu Lys Lys Glu Ser Leu Ile Pro Asp His Gln Asn Lys Glu Leu
 500 505 510

Arg

<210> SEQ ID NO 50
 <211> LENGTH: 513
 <212> TYPE: PRT
 <213> ORGANISM: Vibrio cholerae

<400> SEQUENCE: 50

Met Ala Ser Met Leu His Leu Met Ile Lys Pro Gly Gln Leu Ser Leu
 1 5 10 15
 Lys Gln Leu Arg Gln Val Ser Arg Ser Pro Val Val Leu Ser Leu Asp
 20 25 30
 Pro Glu Ala Ile Pro Ala Ile Ala Glu Ser Ala Gln Val Val Glu Gln
 35 40 45
 Val Ile Ser Glu Gly Arg Thr Val Tyr Gly Ile Asn Thr Gly Phe Gly
 50 55 60
 Leu Leu Ala Asn Thr Lys Ile Ala Pro Gln Asp Leu Glu Thr Leu Gln
 65 70 75 80
 Lys Ser Ile Val Leu Ser His Ala Ala Gly Ile Gly Glu Leu Met Ser
 85 90 95
 Asp Glu Thr Val Arg Leu Met Met Leu Leu Lys Ile Asn Ser Leu Ala
 100 105 110
 Arg Gly Tyr Ser Gly Ile Arg Leu Glu Val Ile Gln Ala Leu Ile Glu
 115 120 125
 Leu Val Asn Asn Gln Ile Tyr Pro Cys Val Pro Lys Lys Gly Ser Val
 130 135 140

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Gly Ala Ser Gly Asp Leu Ala Pro Leu Ala His Met Ser Thr Val Leu
 145 150 155 160
 Leu Gly Glu Gly Gln Ala Arg Asp Tyr Asn Gly Lys Ile Ile Ser Gly
 165 170 175
 Leu Glu Ala Met Lys Ile Ala Gly Leu Glu Pro Ile Thr Leu Ala Pro
 180 185 190
 Lys Glu Gly Leu Ala Leu Leu Asn Gly Thr Gln Ala Ser Thr Ala Phe
 195 200 205
 Ala Leu Glu Gly Leu Phe Val Ala Glu Asp Leu Phe Ala Ser Ala Thr
 210 215 220
 Val Cys Gly Ala Met Ser Val Glu Ala Ala Leu Gly Ser Arg Arg Pro
 225 230 235 240
 Phe Asp Pro Arg Ile His Arg Pro Val Arg Gly His Arg Thr Gln Met
 245 250 255
 Asp Ala Ala Thr Ala Tyr Arg His Leu Leu Val Ser Ser Glu Ile Gly
 260 265 270
 Gln Ser His Ser Asn Cys Glu Gly Lys Val Gln Asp Pro Tyr Ser Leu
 275 280 285
 Arg Cys Gln Pro Gln Val Met Gly Ala Cys Leu Gln Gln Ile Arg Ser
 290 295 300
 Ala Ala Glu Val Leu Glu Val Glu Ala Asn Ser Val Ser Asp Asn Pro
 305 310 315 320
 Leu Val Phe Ala Asp Gly Asp Ile Ile Ser Gly Gly Asn Phe His Ala
 325 330 335
 Glu Pro Val Ala Met Ala Ala Asp Asn Leu Ala Leu Ala Ile Ala Glu
 340 345 350
 Ile Gly Ser Leu Ser Glu Arg Arg Met Ala Leu Leu Ile Asp Ser Ala
 355 360 365
 Leu Ser Lys Asp Leu Pro Pro Phe Leu Val Asp Asn Gly Gly Val Asn
 370 375 380
 Ser Gly Phe Met Ile Ala Gln Val Thr Ala Ala Ala Leu Ala Ser Glu
 385 390 395 400
 Asn Lys Thr Leu Ala His Pro Ala Ser Val Asp Ser Leu Pro Thr Ser
 405 410 415
 Ala Asn Gln Glu Asp His Val Ser Met Ala Thr Phe Ala Ala Arg Arg
 420 425 430
 Leu Arg Asp Met Gly Glu Asn Thr Arg Gly Ile Leu Ala Val Glu Tyr
 435 440 445
 Leu Ala Ala Ala Gln Gly Leu Asp Phe Arg Ala Pro Leu Lys Ser Ser
 450 455 460
 Pro Arg Ile Glu Glu Ala Arg Gln Ile Leu Arg Glu Lys Val Pro Phe
 465 470 475 480
 Tyr Asp Lys Asp Arg Tyr Phe Ala Pro Asp Ile Glu Lys Ala Asn Ala
 485 490 495
 Leu Leu Ala Gln Leu Ala Val His Asn Arg Leu Met Pro Asp Gln Leu
 500 505 510

Leu

<210> SEQ ID NO 51

<211> LENGTH: 513

<212> TYPE: PRT

<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 51

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Met	Ala	Ser	Ala	Met	Ser	Leu	His	Leu	Lys	Pro	Gly	Gln	Leu	Thr	Leu	1	5	10	15
Ala	Asp	Leu	Arg	Gln	Ala	Tyr	Leu	Ala	Pro	Val	Arg	Leu	Ser	Leu	Asp	20	25	30	
Pro	Ser	Ala	Asp	Ala	Pro	Ile	Ala	Ala	Ser	Val	Ala	Cys	Val	Glu	Asn	35	40	45	
Ile	Ile	Ala	Glu	Gly	Arg	Thr	Ala	Tyr	Gly	Ile	Asn	Thr	Gly	Phe	Gly	50	55	60	
Leu	Leu	Ala	Ser	Thr	Arg	Ile	Ser	Pro	Ala	Asp	Leu	Glu	Lys	Leu	Gln	65	70	75	80
Arg	Ser	Ile	Val	Leu	Ser	His	Ala	Ala	Gly	Val	Gly	Glu	Ala	Leu	Asp	85	90	95	
Asp	Ala	Met	Val	Arg	Leu	Val	Met	Leu	Leu	Lys	Val	Asn	Ser	Leu	Ala	100	105	110	
Arg	Gly	Phe	Ser	Gly	Ile	Arg	Arg	Lys	Val	Ile	Asp	Ala	Leu	Ile	Ala	115	120	125	
Leu	Ile	Asn	Ala	Glu	Val	Tyr	Pro	His	Ile	Pro	Leu	Lys	Gly	Ser	Val	130	135	140	
Gly	Ala	Ser	Gly	Asp	Leu	Ala	Pro	Leu	Ala	His	Met	Ser	Leu	Val	Leu	145	150	155	160
Ile	Gly	Glu	Ser	Arg	Ala	Arg	His	Ala	Arg	Gly	Glu	Trp	Leu	Pro	Ala	165	170	175	
Ala	Glu	Ala	Leu	Ala	Val	Ala	Gly	Leu	Glu	Pro	Leu	Thr	Leu	Ala	Ala	180	185	190	
Lys	Glu	Gly	Leu	Ala	Leu	Leu	Asn	Gly	Thr	Gln	Val	Ser	Thr	Ala	Tyr	195	200	205	
Ala	Leu	Arg	Gly	Leu	Phe	Glu	Ala	Glu	Asp	Leu	Phe	Ala	Ala	Ala	Thr	210	215	220	
Val	Cys	Gly	Gly	Leu	Ser	Val	Glu	Ala	Met	Leu	Gly	Ser	Arg	Ala	Pro	225	230	235	240
Phe	Asp	Ala	Arg	Ile	His	Ala	Ala	Leu	Arg	Gly	Gln	Arg	Gly	Gln	Ile	245	250	255	
Asp	Val	Ala	Ala	Ala	Tyr	Arg	Asp	Leu	Leu	Ala	Ser	Ser	Glu	Val	Ala	260	265	270	
Arg	Ser	His	Glu	Lys	Cys	Asp	Gly	Lys	Val	Gln	Asp	Pro	Tyr	Ser	Leu	275	280	285	
Arg	Cys	Gln	Pro	Gln	Val	Met	Gly	Ala	Cys	Leu	Thr	Gln	Met	Arg	Gln	290	295	300	
Ala	Ala	Glu	Val	Leu	Glu	Ile	Glu	Ala	Asn	Ala	Val	Ser	Asp	Asn	Pro	305	310	315	320
Leu	Val	Phe	Ala	Ala	Gly	Asp	Val	Ile	Ser	Gly	Gly	Asn	Phe	His	Ala	325	330	335	
Glu	Pro	Val	Ala	Met	Ala	Ala	Asp	Asn	Leu	Ala	Leu	Ala	Leu	Ala	Glu	340	345	350	
Ile	Gly	Ser	Leu	Ser	Glu	Arg	Arg	Ile	Ser	Leu	Met	Met	Asp	Met	His	355	360	365	
Met	Ser	Gln	Asp	Leu	Pro	Pro	Phe	Leu	Val	Ala	Asn	Gly	Gly	Val	Asn	370	375	380	
Ser	Gly	Phe	Met	Ile	Ala	Gln	Val	Thr	Ala	Ala	Ala	Leu	Ala	Ser	Asp	385	390	395	400
Asn	Lys	Ala	Leu	Ala	His	Pro	Ala	Ser	Val	Asp	Ser	Leu	Pro	Thr	Ser	405	410	415	
Ala	Asn	Gln	Glu	Asp	His	Val	Ser	Met	Ala	Pro	Asn	Ala	Gly	Lys	Arg				

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420	425	430
Leu Trp Ala Met Ala Glu Asn Val Arg Gly Ile Leu Ala Val Glu Trp 435 440 445		
Leu Gly Ala Cys Gln Gly Leu Asp Phe Arg Glu Gly Leu Lys Ser Ser 450 455 460		
Pro Lys Leu Glu Gln Ala Arg Arg Leu Leu Arg Asp Lys Val Pro Tyr 465 470 475 480		
Tyr Gln Glu Asp Arg Phe Phe Ala Pro Asp Ile Glu Ala Ala Ser Gln 485 490 495		
Leu Leu Ala Ser Gly Cys Leu Asn Ala Leu Leu Pro Ala Arg Leu Leu 500 505 510		
Pro		

<210> SEQ ID NO 52

<211> LENGTH: 513

<212> TYPE: PRT

<213> ORGANISM: Bacillus halodurans

<400> SEQUENCE: 52

Met Ala Met Thr Asn Leu Lys Leu Leu Asp Gly Arg Ser Leu Ser Leu 1 5 10 15
His Asp Leu His Arg Ile Ile Tyr Glu Gly Glu Thr Val Gly Ala Ser 20 25 30
Asp Glu Ser Met Glu Lys Val Lys Gln Ser Arg Lys Ala Val Glu Gln 35 40 45
Ile Val Ala Asp Glu Lys Ile Ile Tyr Gly Ile Thr Thr Gly Phe Gly 50 55 60
Lys Phe Ser Asp Ile Phe Ile Asp Pro Asp Asp Val Glu Asn Leu Gln 65 70 75 80
His Asn Leu Ile Tyr Ser His Ala Cys Gly Val Gly Ser Pro Phe Pro 85 90 95
Glu Thr Val Ser Arg Thr Met Leu Val Leu Arg Ala Asn Ala Leu Leu 100 105 110
Lys Gly Phe Ser Gly Val Arg Pro Leu Val Ile Glu Arg Leu Leu Ala 115 120 125
Leu Val Asn Ala Asn Ile His Pro Val Ile Pro Gln Gln Gly Ser Leu 130 135 140
Gly Ala Ser Gly Asp Leu Ala Pro Leu Ser His Leu Ala Leu Val Leu 145 150 155 160
Leu Gly Glu Gly Glu Val Phe Asp Tyr Lys Gly Thr Lys Thr Lys Ala 165 170 175
Ser Phe Ala Leu Lys Glu Glu Glu Ile Glu Pro Ile Thr Leu Thr Ala 180 185 190
Lys Glu Gly Leu Ala Leu Ile Asn Gly Thr Gln Ala Met Thr Ala Met 195 200 205
Gly Val Ile Ala Tyr Leu Glu Ala Glu Lys Leu Ala Phe Gln Ser Glu 210 215 220
Ile Ile Ala Ser Leu Thr Met Glu Gly Leu Arg Gly Ile Ile Asp Ala 225 230 235 240
Phe Asp Glu Gln Ile His Phe Ala Leu Arg Gly Tyr Val Glu Gln Val 245 250 255
Asp Val Ala Arg Arg Met Glu Ser Tyr Leu Gln Asp Ser Gln Leu Thr 260 265 270
Thr Ser His Arg Gln Gly Glu Leu Arg Val Gln Asp Ala Tyr Ser Leu

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275					280					285					
Arg	Cys	Ile	Pro	Gln	Val	His	Gly	Ala	Thr	Trp	Gln	Thr	Leu	Arg	Tyr
290						295					300				
Val	Lys	Glu	Lys	Leu	Glu	Ile	Glu	Met	Asn	Ala	Ala	Thr	Asp	Asn	Pro
305					310					315					320
Leu	Ile	Phe	Asp	Asn	Gly	Gln	Val	Ile	Ser	Gly	Gly	Asn	Phe	His	Gly
				325					330					335	
Gln	Gln	Ile	Ala	Leu	Ala	Met	Asp	Phe	Leu	Gly	Ile	Ala	Met	Ala	Glu
			340					345					350		
Leu	Ala	Asn	Ile	Ser	Glu	Arg	Arg	Ile	Glu	Arg	Leu	Val	Asn	Pro	Gln
		355					360					365			
Leu	Asn	Arg	Asp	Leu	Pro	Pro	Phe	Leu	Ser	Ala	Ala	Pro	Gly	Val	Gln
370						375					380				
Ser	Gly	Val	Met	Ile	Leu	Gln	Tyr	Cys	Ala	Ala	Ser	Leu	Val	Ser	Glu
385					390					395					400
Asn	Lys	Thr	Leu	Ala	His	Pro	Ala	Ser	Val	Asp	Ser	Ile	Pro	Ser	Ser
				405					410					415	
Ala	Asn	Gln	Glu	Asp	His	Val	Ser	Met	Gly	Thr	Ile	Gly	Ser	Arg	His
			420					425					430		
Ala	Tyr	Gln	Ile	Ile	Gln	Asn	Val	Arg	Asn	Val	Leu	Ala	Ile	Glu	Leu
		435					440					445			
Ile	Cys	Ala	Met	Gln	Ala	Val	Asp	Ile	Arg	Gly	Arg	Glu	Lys	Met	Ala
450						455					460				
Ser	Phe	Thr	Lys	Lys	Ile	Leu	Glu	Lys	Gly	Arg	Glu	His	Val	Pro	Tyr
465					470					475					480
Ile	Asp	Gln	Asp	Arg	Met	Phe	Ala	Lys	Asp	Ile	Glu	Arg	Ala	Ala	Lys
				485					490					495	
Trp	Leu	Lys	Asp	Gly	Ser	Trp	Asp	Phe	Thr	Lys	Met	Arg	Glu	Lys	Glu
			500					505					510		

Arg

<210> SEQ ID NO 53

<211> LENGTH: 513

<212> TYPE: PRT

<213> ORGANISM: Pseudomonas putida

<400> SEQUENCE: 53

Met	Ala	Ser	Ala	Thr	Glu	Leu	Thr	Leu	Lys	Pro	Gly	Thr	Leu	Thr	Leu
1				5					10					15	
Ala	Gln	Leu	Arg	Ala	Ile	His	Ala	Ala	Pro	Val	Arg	Leu	Gln	Leu	Asp
			20					25					30		
Ala	Ser	Ala	Ala	Pro	Ala	Ile	Asp	Ala	Ser	Val	Ala	Cys	Val	Glu	Gln
		35					40					45			
Ile	Ile	Ala	Glu	Asp	Arg	Thr	Ala	Tyr	Gly	Ile	Asn	Thr	Gly	Phe	Gly
		50				55					60				
Leu	Leu	Ala	Ser	Thr	Arg	Ile	Ala	Ser	His	Asp	Leu	Glu	Asn	Leu	Gln
65					70					75					80
Arg	Ser	Leu	Val	Leu	Ser	His	Ala	Ala	Gly	Ile	Gly	Ala	Pro	Leu	Asp
				85					90					95	
Asp	Asp	Leu	Val	Arg	Leu	Ile	Met	Val	Leu	Lys	Ile	Asn	Ser	Leu	Ser
		100						105					110		
Arg	Gly	Phe	Ser	Gly	Ile	Arg	Arg	Lys	Val	Ile	Asp	Ala	Leu	Ile	Ala
		115					120					125			
Leu	Val	Asn	Ala	Glu	Val	Tyr	Pro	His	Ile	Pro	Leu	Lys	Gly	Ser	Val

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130	135	140
Gly Ala Ser Gly Asp 145	Leu Ala Pro Leu Ala His Met Ser Leu Val Leu 150	155
Leu Gly Glu Gly Lys Ala Arg Asp Tyr Lys Gly Gln Trp Leu Ser Ala 165	170	175
Thr Glu Ala Leu Ala Val Ala Gly Leu Glu Pro Leu Thr Leu Ala Ala 180	185	190
Lys Glu Gly Leu Ala Leu Leu Asn Gly Thr Gln Ala Ser Thr Ala Tyr 195	200	205
Ala Leu Arg Gly Leu Phe Tyr Ala Glu Asp Leu Tyr Ala Ala Ala Ile 210	215	220
Ala Cys Gly Gly Leu Ser Val Glu Ala Val Leu Gly Ser Arg Ser Pro 225	230	235
Phe Asp Ala Arg Ile His Glu Ala Leu Arg Gly Gln Arg Gly Gln Ile 245	250	255
Asp Thr Ala Ala Cys Phe Arg Asp Leu Leu Gly Asp Ser Ser Glu Val 260	265	270
Ser Ser His Lys Asn Cys Asp Gly Lys Val Gln Asp Pro Tyr Ser Leu 275	280	285
Arg Cys Gln Pro Gln Val Met Gly Ala Cys Leu Thr Gln Leu Arg Gln 290	295	300
Ala Ala Glu Val Leu Gly Ile Glu Ala Asn Ala Val Ser Asp Asn Pro 305	310	315
Leu Val Phe Ala Ala Gly Asp Val Ile Ser Gly Gly Asn Phe His Ala 325	330	335
Glu Pro Val Ala Met Ala Ala Asp Asn Leu Ala Leu Ala Ile Ala Glu 340	345	350
Ile Gly Ser Leu Ser Glu Arg Arg Ile Ser Leu Met Met Asp Lys His 355	360	365
Met Ser Gln Asp Leu Pro Pro Phe Leu Val Glu Asn Gly Gly Val Asn 370	375	380
Ser Gly Phe Met Ile Ala Gln Val Thr Ala Ala Ala Leu Ala Ser Glu 385	390	395
Asn Lys Ala Leu Ser His Pro His Ser Val Asp Ser Leu Pro Thr Ser 405	410	415
Ala Asn Gln Glu Asp His Val Ser Met Ala Pro Ala Ala Gly Lys Arg 420	425	430
Leu Trp Glu Met Ala Glu Asn Thr Arg Gly Val Leu Ala Ile Glu Trp 435	440	445
Leu Gly Ala Cys Gln Gly Leu Asp Leu Arg Lys Gly Leu Lys Thr Ser 450	455	460
Ala Lys Leu Glu Lys Ala Arg Gln Ala Leu Arg Ser Glu Val Ala His 465	470	475
Tyr Asp Arg Asp Arg Phe Phe Ala Pro Asp Ile Glu Lys Ala Val Glu 485	490	495
Leu Leu Ala Lys Gly Ser Leu Thr Gly Leu Leu Pro Ala Gly Leu Pro 500	505	510
Ser		

<210> SEQ ID NO 54

<211> LENGTH: 513

<212> TYPE: PRT

<213> ORGANISM: Rhizobium meliloti

-continued

<400> SEQUENCE: 54

Met Ala Ser Ala Pro Gln Ile Thr Leu Arg Pro Gly Ser Val Pro Leu
 1 5 10 15
 Ser Asp Leu Glu Thr Ile Tyr Trp Thr Gly Ala Pro Ala Arg Leu Asp
 20 25 30
 Ala Ala Phe Asp Ala Gly Ile Ala Lys Ala Ala Ala Arg Ile Ala Glu
 35 40 45
 Ile Val Ala Gly Asn Ala Pro Val Tyr Gly Ile Asn Thr Gly Phe Gly
 50 55 60
 Lys Leu Ala Ser Ile Lys Ile Asp Ser Ser Asp Val Ala Thr Leu Gln
 65 70 75 80
 Arg Asn Leu Ile Leu Ser His Cys Cys Gly Val Gly Gln Pro Leu Thr
 85 90 95
 Glu Asp Ile Val Arg Leu Ile Met Ala Leu Lys Leu Ile Ser Leu Gly
 100 105 110
 Arg Gly Ala Ser Gly Val Arg Leu Glu Leu Val Arg Leu Ile Glu Ala
 115 120 125
 Met Leu Asp Lys Gly Val Ile Pro Leu Ile Pro Glu Lys Gly Ser Val
 130 135 140
 Gly Ala Ser Gly Asp Leu Ala Pro Leu Ala His Met Ala Ala Val Met
 145 150 155 160
 Met Gly His Gly Glu Ala Phe Phe Ala Gly Glu Arg Met Lys Gly Asp
 165 170 175
 Ala Ala Leu Lys Ala Glu Ala Gly Leu Ser Pro Val Thr Leu Ala Ala
 180 185 190
 Lys Glu Gly Leu Ala Leu Ile Asn Gly Thr Gln Val Ser Thr Ala Leu
 195 200 205
 Ala Leu Ala Gly Leu Phe Arg Ala His Arg Ala Gly Gln Ala Ala Leu
 210 215 220
 Ile Thr Gly Ala Leu Ser Thr Asp Ala Ala Met Gly Ser Ser Ala Pro
 225 230 235 240
 Phe His Pro Asp Ile Gln His Cys Ala Ala Ile Arg Ala Arg Ser Thr
 245 250 255
 Arg Ala Ala Ala Asn Leu Arg Gln Leu Leu Thr Gly Ser Pro Ile Arg
 260 265 270
 Gln Ser His Ile Glu Gly Asp Glu Arg Val Gln Asp Pro Tyr Cys Ile
 275 280 285
 Arg Cys Gln Pro Gln Val Asp Gly Ala Cys Leu Asp Leu Leu Arg Ser
 290 295 300
 Val Ala Ala Thr Leu Thr Ile Glu Ala Asn Ala Val Thr Asp Asn Pro
 305 310 315 320
 Leu Val Leu Ser Asp Asn Ser Val Val Ser Gly Gly Asn Phe His Ala
 325 330 335
 Glu Pro Val Ala Phe Ala Ala Asp Gln Ile Ala Leu Ala Val Cys Glu
 340 345 350
 Ile Gly Ala Ile Ser Gln Arg Arg Ile Ala Leu Leu Val Asp Pro Ala
 355 360 365
 Leu Ser Leu Arg Leu Pro Ala Phe Leu Ala Lys Lys Pro Gly Leu Asn
 370 375 380
 Ser Gly Leu Met Ile Ala Glu Val Thr Ser Ala Ala Leu Met Ser Glu
 385 390 395 400
 Asn Lys Gln Leu Ser His Pro Ala Ser Val Asp Ser Thr Pro Thr Ser
 405 410 415

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Ala Asn Gln Glu Asp His Val Ser Met Ala Cys His Gly Ala Arg Arg
 420 425 430
 Leu Leu Gln Met Thr Glu Asn Leu Phe Ser Ile Ile Gly Ile Glu Ala
 435 440 445
 Leu Ala Ala Val Gln Gly Ile Glu Phe Arg Ala Pro Leu Thr Thr Ser
 450 455 460
 Pro Glu Leu Gln Lys Ala Ala Ala Ala Val Arg Gly Val Ser Ser Ser
 465 470 475 480
 Ile Glu Glu Asp Arg Tyr Met Ala Asp Asp Leu Lys Ala Ala Gly Asp
 485 490 495
 Leu Val Ala Ser Gly Arg Leu Ala Ala Val Ser Ala Gly Leu Pro
 500 505 510

Lys

<210> SEQ ID NO 55
 <211> LENGTH: 513
 <212> TYPE: PRT
 <213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 55

Met Ser Asp Leu Pro Ser Val Val Phe Gly Asp Gly Pro Leu Arg Trp
 1 5 10 15
 Gln Glu Leu Val Ala Val Ala Arg His Gly Ala Arg Leu Glu Leu Ser
 20 25 30
 Ala Ala Ala Trp Ala Arg Ile Asp Asn Ala Arg Ala Ile Val Cys Arg
 35 40 45
 Ile Val Ala Asn Gly Glu Arg Ala Tyr Gly Ile Ser Thr Gly Leu Gly
 50 55 60
 Ala Leu Cys Asp Val Leu Leu Glu Gly Glu Gln Leu Ala Glu Leu Ser
 65 70 75 80
 Arg Asn Thr Leu Leu Ser His Ala Cys Gly Val Gly Glu Pro Leu Arg
 85 90 95
 Asp Glu Gln Thr Arg Ala Ile Ile Cys Ala Ala Val Ala Asn Tyr Ser
 100 105 110
 Gln Gly Lys Ser Gly Leu Asp Arg Ser Leu Val Glu Gly Leu Leu Ala
 115 120 125
 Leu Leu Asn His Gly Ile Thr Pro Gln Val Pro Ala Gln Gly Ser Val
 130 135 140
 Gly Tyr Ser Gly Asp Leu Thr His Met Ala His Val Gly Ile Ala Leu
 145 150 155 160
 Leu Gly Ile Gly Glu Val Ser Asp Tyr Arg Gly Ser Val Val Pro Ala
 165 170 175
 Ala Ala Ala Leu Ala Ala Glu Gly Leu Ala Thr Val Arg Leu Gly Ala
 180 185 190
 Lys Asp Gly Leu Cys Leu Val Asn Gly Thr Pro Cys Met Thr Gly Leu
 195 200 205
 Ala Cys Leu Ala Leu Asp Asp Ala Gln Arg Leu Ala Gln Trp Ala Asp
 210 215 220
 Val Ile Gly Ala Met Ser Phe Glu Ala Leu Arg Gly Gln Leu Ala Ala
 225 230 235 240
 Phe Asp Ala Glu Ile His Val Ala Leu Lys Pro His Pro Gly Met Gln
 245 250 255
 Arg Val Ala Ala Asn Leu Arg Ala Leu Leu Ala Gly Ser Gln Val Leu
 260 265 270

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Glu Asn Ala Arg Glu Gly Gly Ile Arg Thr Gln Asp Ala Leu Ser Ile
 275 280 285
 Arg Ser Ile Pro Gln Ile His Gly Ala Cys Arg Asp Gln Leu Ala His
 290 295 300
 Ala Arg Gln Ile Glu Thr Arg Glu Leu Asn Ser Ala Thr Asp Asn Pro
 305 310 315 320
 Leu Leu Leu Gly Thr Pro Glu Val Val Ser Gln Ala Asn Pro His Gly
 325 330 335
 Glu Ser Val Ala Met Ala Ala Asp Leu Leu Ala Ile Ala Val Ala Glu
 340 345 350
 Leu Gly Gly Val Ala Glu Arg Arg Leu Asp Arg Leu Val Asn Pro Leu
 355 360 365
 Val Ser Arg Gly Leu Pro Ala Phe Leu Val Gly Lys Pro Gly Val Asn
 370 375 380
 Ser Gly Met Met Ile Thr Gln Tyr Val Ala Ala Ser Leu Ala Gly Glu
 385 390 395 400
 Asn Arg Gln Leu Ala Gln Pro Ala Val Val Asp Asn Phe Val Thr Ser
 405 410 415
 Ala Leu Gln Glu Asp His Leu Ser Leu Gly Thr Ser Ala Ala Leu Lys
 420 425 430
 Leu Gly Arg Ala Leu Glu Asn Leu Arg Arg Ile Leu Ala Ile Glu Tyr
 435 440 445
 Leu Leu Ala Ala Gln Ala Phe Glu Phe Leu Ala Pro Gln Arg Phe Gly
 450 455 460
 Gln Gly Thr Ala Ala Ala Trp Gly Ile Leu Arg Glu Arg Val Pro Ala
 465 470 475 480
 Tyr Asp Thr Asp Arg Trp Leu Ala Pro Asp Ile Ala Ser Ala Ala Ala
 485 490 495
 Ile Leu Gly Glu Arg Lys Ser Leu Ala Arg Leu Ala Ala Ser Ile Gly
 500 505 510

Asp

<210> SEQ ID NO 56
 <211> LENGTH: 513
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 56

Lys Tyr Arg Glu Pro Glu Lys Tyr Ile Glu Leu Asp Gly Leu Thr Thr
 1 5 10 15
 Glu Asp Leu Val Asn Leu Gly Lys Gly Arg Tyr Lys Ile Lys Leu Thr
 20 25 30
 Pro Thr Ala Glu Lys Arg Val Gln Lys Ser Arg Glu Val Ile Asp Ser
 35 40 45
 Ile Ile Lys Glu Lys Thr Val Val Tyr Gly Ile Thr Thr Gly Phe Gly
 50 55 60
 Lys Phe Ala Thr Arg Thr Val Ile Pro Ile Asn Lys Leu Gln Leu Gln
 65 70 75 80
 Val Asn Leu Val Arg Ser His Ser Ser Gly Val Gly Lys Pro Leu Ser
 85 90 95
 Pro Glu Arg Cys Arg Met Leu Leu Ala Leu Arg Ile Asn Val Leu Ala
 100 105 110
 Lys Gly Tyr Ser Gly Ile Ser Leu Glu Thr Leu Lys Gln Val Ile Glu
 115 120 125

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Met Phe Asn Ala Ser Cys Leu Pro Tyr Val Pro Glu Lys Gly Thr Val
 130 135 140

Gly Ala Ser Gly Asp Leu Ala Pro Leu Ser His Leu Ala Leu Gly Leu
 145 150 155 160

Val Gly Glu Gly Lys Met Trp Ser Pro Lys Ser Gly Trp Ala Asp Ala
 165 170 175

Lys Tyr Val Leu Glu Ala His Gly Leu Lys Pro Val Ile Leu Lys Pro
 180 185 190

Lys Glu Gly Leu Ala Leu Ile Asn Gly Thr Gln Met Ile Thr Ser Leu
 195 200 205

Gly Cys Glu Ala Val Glu Arg Ala Ser Ala Ile Ala Arg Gln Ala Asp
 210 215 220

Ile Val Ala Ala Leu Thr Leu Glu Val Leu Lys Gly Thr Thr Lys Ala
 225 230 235 240

Phe Asp Thr Asp Ile His Ala Pro Leu Arg Pro His Arg Gly Gln Ile
 245 250 255

Glu Val Ala Phe Arg Phe Arg Ser Leu Leu Ser Asp Ser Glu Ile Ala
 260 265 270

Glu Ser His Arg Phe Cys Asp Gly Arg Val Gln Asp Ala Tyr Thr Leu
 275 280 285

Arg Cys Cys Pro Gln Val His Gly Val Val Asn Asp Thr Ile Ala Phe
 290 295 300

Val Lys Asn Ile Ile Thr Thr Glu Leu Asn Ser Ala Thr Asp Asn Pro
 305 310 315 320

Met Val Phe Ala Asn Gly Glu Thr Val Ser Gly Gly Asn Phe His Gly
 325 330 335

Glu Tyr Pro Ala Lys Ala Leu Asp Tyr Leu Ala Ile Gly Ile His Glu
 340 345 350

Leu Ala Ala Ile Ser Glu Arg Arg Ile Glu Arg Leu Cys Asn Pro Ser
 355 360 365

Leu Ser Arg Glu Leu Pro Ala Phe Leu Val Ala Glu Gly Gly Leu Asn
 370 375 380

Ser Gly Phe Met Ile Ala His Cys Thr Ala Ala Ala Leu Val Ser Glu
 385 390 395 400

Asn Lys Ala Leu Cys His Pro Ser Ser Val Asp Ser Leu Ser Thr Ser
 405 410 415

Ala Ala Thr Glu Asp His Val Ser Met Gly Gly Trp Ala Ala Arg Lys
 420 425 430

Ala Leu Arg Val Ile Glu His Val Glu Gln Val Leu Ala Ile Glu Leu
 435 440 445

Leu Ala Ala Cys Gln Gly Ile Glu Phe Leu Arg Pro Leu Lys Thr Thr
 450 455 460

Thr Pro Leu Glu Lys Val Tyr Asp Leu Val Arg Ser Val Val Arg Pro
 465 470 475 480

Trp Ile Lys Asp Arg Phe Met Ala Pro Asp Ile Glu Ala Ala His Arg
 485 490 495

Leu Leu Leu Glu Gln Lys Val Trp Glu Val Ala Ala Pro Tyr Ile Glu
 500 505 510

Lys

<210> SEQ ID NO 57
 <211> LENGTH: 513
 <212> TYPE: PRT

-continued

<213> ORGANISM: *Caenorhabditis elegans*

<400> SEQUENCE: 57

Val Leu Ala Pro Pro Thr Lys Leu Leu Ile Leu Asp Gly Asn Ser Pro
 1 5 10 15
 Glu Asp Leu Val Arg Cys Glu Lys Gly Glu Cys Ala Ile Gln Leu Ser
 20 25 30
 Met Glu Ser Glu Asp Arg Ile Arg Lys Ala Arg Thr Phe Leu Glu Lys
 35 40 45
 Ile Ala Ser Glu His Arg Ala Val Tyr Gly Val Thr Thr Gly Phe Gly
 50 55 60
 Thr Phe Ser Asn Val Thr Ile Pro Pro Glu Lys Leu Lys Lys Leu Gln
 65 70 75 80
 Leu Asn Leu Ile Arg Ser His Ala Thr Gly Tyr Gly Glu Pro Leu Ala
 85 90 95
 Pro Asn Arg Ala Arg Met Leu Leu Ala Leu Arg Ile Asn Ile Leu Ala
 100 105 110
 Lys Gly His Ser Gly Ile Ser Val Glu Asn Ile Lys Lys Met Ile Ala
 115 120 125
 Ala Phe Asn Ala Phe Cys Val Ser Tyr Val Pro Gln Gln Gly Thr Val
 130 135 140
 Gly Cys Ser Gly Asp Leu Cys Pro Leu Ala His Leu Ala Leu Gly Leu
 145 150 155 160
 Leu Gly Glu Gly Lys Met Trp Ser Pro Thr Thr Gly Trp Gln Pro Ala
 165 170 175
 Asp Val Val Leu Lys Lys Asn Asn Leu Glu Pro Leu Glu Leu Gly Pro
 180 185 190
 Lys Glu Gly Leu Ala Leu Ile Asn Gly Thr Gln Met Val Thr Ala Leu
 195 200 205
 Gly Ala Tyr Thr Leu Glu Arg Ala His Asn Ile Ala Arg Gln Ala Asp
 210 215 220
 Val Ile Ala Ala Leu Ser Leu Asp Val Leu Lys Gly Thr Thr Arg Ala
 225 230 235 240
 Tyr Asp Pro Asp Ile His Arg Pro Ile Arg Pro His Arg Gly Gln Asn
 245 250 255
 Leu Ser Ala Leu Arg Leu Arg Ala Leu Leu Asn Pro Ser Gln Ile Ala
 260 265 270
 Glu Ser His Arg Asn Cys Thr Gly Lys Val Gln Asp Ala Tyr Thr Leu
 275 280 285
 Arg Cys Val Pro Gln Val His Gly Val Val His Asp Thr Ile Glu Phe
 290 295 300
 Val Arg Glu Ile Ile Thr Thr Glu Met Asn Ser Ala Thr Asp Asn Pro
 305 310 315 320
 Leu Val Phe Ala Asp Arg Glu Ile Ile Ser Gly Gly Asn Phe His Gly
 325 330 335
 Glu Tyr Pro Ala Lys Ala Leu Asp Phe Leu Ala Ile Ala Val Ala Glu
 340 345 350
 Leu Ala Gln Met Ser Glu Arg Arg Leu Glu Arg Leu Val Asn Lys Glu
 355 360 365
 Leu Ser Arg Gly Leu Pro Thr Phe Leu Thr Pro Asp Gly Gly Leu Asn
 370 375 380
 Ser Gly Phe Met Thr Val Gln Leu Cys Ala Ala Ser Leu Val Ser Glu
 385 390 395 400

-continued

Asn Lys Val Leu Cys His Pro Ser Ser Val Asp Ser Ile Pro Thr Ser
 405 410 415
 Cys Asn Gln Glu Asp His Val Ser Met Gly Gly Phe Ala Ala Arg Lys
 420 425 430
 Ala Leu Thr Val Val Glu His Val Glu Ala Val Leu Ala Met Glu Leu
 435 440 445
 Leu Ala Ala Cys Gln Gly Ile Glu Phe Leu Lys Pro Leu Ile Ser Thr
 450 455 460
 Ala Pro Leu His Lys Ile Tyr Gln Leu Val Arg Ser Lys Val Ala Pro
 465 470 475 480
 Pro Asn Glu Asp Arg Tyr Met Lys Pro Glu Ile Asp Ala Val Leu Glu
 485 490 495
 Met Ile Arg Glu Asn Arg Ile Trp Glu Ala Val Leu Pro His Leu Glu
 500 505 510
 Thr

<210> SEQ ID NO 58
 <211> LENGTH: 513
 <212> TYPE: PRT
 <213> ORGANISM: Thermoplasma acidophilum

<400> SEQUENCE: 58

Met Ala Ser Ala Pro Met Ile Glu Ile Asp Gly Arg Ser Leu Arg Val
 1 5 10 15
 Glu Asp Val Tyr Ala Val Ala Val Glu Tyr Asp Arg Val Ser Ile Ser
 20 25 30
 Asp Asp Thr Leu Lys Ala Val Glu Glu Lys His Glu Ala Phe Leu Lys
 35 40 45
 Leu Ile Asn Ser Gly Lys Thr Val Tyr Gly Val Asn Thr Gly Phe Gly
 50 55 60
 Ser Leu Leu Asn Val His Ile Glu Arg Asp Gln Glu Ile Glu Leu Gln
 65 70 75 80
 Lys Asn Leu Ile Arg Ser His Ser Ser Gly Val Gly Asp Tyr Leu Glu
 85 90 95
 Asn Arg Tyr Val Arg Ala Ile Met Ala Val Arg Leu Asn Ser Leu Ala
 100 105 110
 Ala Gly Tyr Ser Ala Val Ser Ala Asp Leu Leu Asn Met Met Val Glu
 115 120 125
 Met Leu Asn Arg Asp Val Ile Pro Ala Val Pro Lys Tyr Gly Ser Val
 130 135 140
 Gly Ala Ser Gly Asp Leu Ala Pro Leu Ala His Ile Gly Leu Ala Met
 145 150 155 160
 Met Gly Glu Gly Lys Ala Phe Asp Phe Glu Gly Arg Leu Met Asp Ser
 165 170 175
 Ala Arg Ala Leu Glu Lys Ala Gly Leu Lys Pro Tyr Gln Phe Lys Glu
 180 185 190
 Lys Glu Gly Val Ala Leu Ile Asn Gly Thr Ser Phe Met Ser Gly Ile
 195 200 205
 Leu Ser Ile Ala Val Met Asp Ala His Asp Ile Leu Glu Asn Ala Ile
 210 215 220
 Arg Ser Ala Leu Leu Ser Phe Glu Ala Leu Gly Gly Thr Ser Lys Ala
 225 230 235 240
 Phe Thr Pro Trp Ile Leu Gly Ala Leu Arg Pro His Leu Gly Gln Val
 245 250 255

-continued

Ala Ile Gly Asn Arg Phe Arg Glu Tyr Leu Thr Gly Ser Asp Ile Val
 260 265 270

Ala Ser Lys Arg Ala Asp Ser Val Lys Val Gln Asp Ala Tyr Thr Leu
 275 280 285

Arg Cys Ile Pro Gln Val Tyr Gly Ser Val Ala Asp Val Ile Asp Tyr
 290 295 300

Val Glu Asn Val Leu Ser Val Glu Ile Asn Ser Ala Thr Asp Asn Pro
 305 310 315 320

Leu Val Phe Asn Gly Glu Glu Val Val Ser Gly Gly Asn Phe His Gly
 325 330 335

Glu Pro Val Ala Leu Ala Ala Asp Phe Leu Ala Ile Ala Leu Thr Asp
 340 345 350

Leu Gly Asn Met Val Glu Arg Arg Ile Ala Arg Leu Val Asp Thr Asn
 355 360 365

Leu Ser Arg Gly Leu Pro Pro Phe Leu Thr Pro Asp Ser Gly Leu Asn
 370 375 380

Ser Gly Tyr Met Ile Pro Gln Tyr Thr Ala Ala Ala Leu Cys Asn Arg
 385 390 395 400

Asn Lys Val Leu Ala Tyr Pro Ser Ser Ala Asp Thr Ile Pro Thr Ser
 405 410 415

Ala Asn Gln Glu Asp His Val Ser Met Gly Ala Thr Gly Ser Leu Lys
 420 425 430

Leu Leu Glu Ile Ile Asp Asn Val Arg Tyr Ile Ile Ala Ile Glu Tyr
 435 440 445

Leu Leu Gly Ser Gln Ala Leu Glu Phe Thr Asp Lys Leu Gly Met Ser
 450 455 460

Pro Ser Thr Arg Lys Ile Tyr Glu Lys Ile Arg Glu Lys Val Glu Lys
 465 470 475 480

Leu Asp His Asp Arg Pro Pro Ser Phe Asp Ile Glu Thr Ile Arg Lys
 485 490 495

Met Met Asp Lys Lys Glu Phe Ile Ser Ala Leu Pro Ala His Leu Pro
 500 505 510

Ala

<210> SEQ ID NO 59
 <211> LENGTH: 513
 <212> TYPE: PRT
 <213> ORGANISM: Mus sp.

<400> SEQUENCE: 59

Lys Tyr Arg Glu Pro Glu Lys Tyr Ile Ala Leu Asp Gly Asp Ser Thr
 1 5 10 15

Glu Asp Leu Val Asn Leu Gly Lys Gly Arg Tyr Lys Ile Lys Leu Thr
 20 25 30

Ser Ile Ala Glu Lys Lys Val Gln Gln Ser Arg Glu Val Ile Asp Ser
 35 40 45

Ile Ile Lys Glu Arg Thr Val Val Tyr Gly Ile Thr Thr Gly Phe Gly
 50 55 60

Lys Phe Ala Thr Arg Thr Val Ile Pro Ala Asn Lys Leu Gln Leu Gln
 65 70 75 80

Val Asn Leu Val Arg Ser His Ser Ser Gly Val Gly Lys Pro Leu Ser
 85 90 95

Pro Glu Arg Cys Arg Met Leu Leu Ala Leu Arg Ile Asn Val Leu Ala
 100 105 110

-continued

Lys Gly Tyr Ser Gly Ile Ser Leu Glu Thr Leu Lys Gln Val Ile Glu
 115 120 125
 Ala Phe Asn Ala Ser Cys Leu Ser Tyr Val Pro Glu Lys Gly Thr Val
 130 135 140
 Gly Ala Ser Gly Asp Leu Ala Pro Leu Ser His Leu Ala Leu Gly Leu
 145 150 155 160
 Ile Gly Glu Gly Lys Met Trp Ser Pro Lys Ser Gly Trp Ala Asp Ala
 165 170 175
 Lys Tyr Val Leu Glu Ala His Gly Leu Lys Pro Ile Val Leu Lys Pro
 180 185 190
 Lys Glu Gly Leu Ala Leu Ile Asn Gly Thr Gln Met Ile Thr Ser Leu
 195 200 205
 Gly Cys Glu Ala Leu Glu Arg Ala Ser Ala Ile Ala Arg Gln Ala Asp
 210 215 220
 Ile Val Ala Ala Leu Thr Leu Glu Val Leu Lys Gly Thr Thr Lys Ala
 225 230 235 240
 Phe Asp Thr Asp Ile His Ala Pro Val Arg Pro His Arg Gly Gln Ile
 245 250 255
 Glu Val Ala Phe Arg Phe Arg Ser Leu Leu Ser Asp Ser Glu Ile Ala
 260 265 270
 Glu Ser His Arg Phe Cys Asp Gly Arg Val Gln Asp Ala Tyr Thr Leu
 275 280 285
 Arg Cys Cys Pro Gln Val His Gly Val Val Asn Asp Thr Ile Ala Phe
 290 295 300
 Val Lys Asp Ile Ile Thr Thr Glu Leu Asn Ser Ala Thr Asp Asn Pro
 305 310 315 320
 Met Val Phe Ala Ser Gly Glu Thr Ile Ser Gly Gly Asn Phe His Gly
 325 330 335
 Glu Tyr Pro Ala Lys Ala Leu Asp Tyr Leu Ala Ile Gly Val His Glu
 340 345 350
 Leu Ala Ala Ile Ser Glu Arg Arg Ile Glu Arg Leu Cys Asn Pro Ser
 355 360 365
 Leu Ser Arg Glu Leu Pro Ala Phe Leu Val Ala Glu Gly Gly Leu Asn
 370 375 380
 Ser Gly Phe Met Ile Ala His Cys Thr Ala Ala Ala Leu Val Ser Glu
 385 390 395 400
 Ser Lys Ala Leu Cys His Pro Ser Ser Val Asp Ser Leu Ser Thr Ser
 405 410 415
 Ala Ala Thr Glu Asp His Val Ser Met Gly Gly Trp Ala Ala Arg Lys
 420 425 430
 Ala Leu Arg Val Val Glu His Val Glu Gln Val Leu Ala Ile Glu Leu
 435 440 445
 Leu Ala Ala Cys Gln Gly Ile Glu Phe Leu Arg Pro Leu Lys Thr Thr
 450 455 460
 Thr Pro Leu Glu Lys Val Tyr Asp Leu Val Arg Ser Val Val Arg Pro
 465 470 475 480
 Trp Ile Lys Asp Arg Phe Met Ala Pro Asp Ile Glu Ala Ala His Arg
 485 490 495
 Leu Leu Leu Asp Gln Lys Val Trp Glu Val Ala Ala Pro Tyr Ile Glu
 500 505 510

Lys

-continued

<211> LENGTH: 513
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus

 <400> SEQUENCE: 60

 Lys Tyr Arg Glu Pro Glu Lys Tyr Ile Ala Leu Asp Gly Asp Ser Thr
 1 5 10 15
 Glu Asp Leu Val Asn Leu Gly Lys Gly Arg Tyr Lys Ile Lys Leu Thr
 20 25 30
 Ser Ile Ala Glu Lys Lys Val Gln Gln Ser Arg Glu Val Ile Asp Ser
 35 40 45
 Ile Ile Lys Glu Arg Thr Val Val Tyr Gly Ile Thr Thr Gly Phe Gly
 50 55 60
 Lys Phe Ala Thr Arg Thr Val Ile Pro Ala Asn Lys Leu Gln Leu Gln
 65 70 75 80
 Val Asn Leu Val Arg Ser His Ser Ser Gly Val Gly Lys Pro Leu Ser
 85 90 95
 Pro Glu Arg Cys Arg Met Leu Leu Ala Leu Arg Ile Asn Val Leu Ala
 100 105 110
 Lys Gly Tyr Ser Gly Ile Ser Leu Glu Thr Leu Lys Gln Val Ile Glu
 115 120 125
 Ala Phe Asn Ala Ser Cys Leu Ser Tyr Val Pro Glu Lys Gly Thr Val
 130 135 140
 Gly Ala Ser Gly Asp Leu Ala Pro Leu Ser His Leu Ala Leu Gly Leu
 145 150 155 160
 Ile Gly Glu Gly Lys Met Trp Ser Pro Lys Ser Gly Trp Ala Asp Ala
 165 170 175
 Lys Tyr Val Leu Glu Ala His Gly Leu Lys Pro Ile Val Leu Lys Pro
 180 185 190
 Lys Glu Gly Leu Ala Leu Ile Asn Gly Thr Gln Met Ile Thr Ser Leu
 195 200 205
 Gly Cys Glu Ala Leu Glu Arg Ala Ser Ala Ile Ala Arg Gln Ala Asp
 210 215 220
 Ile Val Ala Ala Leu Thr Leu Glu Val Leu Lys Gly Thr Thr Lys Ala
 225 230 235 240
 Phe Asp Thr Asp Ile His Ala Pro Val Arg Pro His Arg Gly Gln Ile
 245 250 255
 Glu Val Ala Phe Arg Phe Arg Ser Leu Leu Ser Asp Ser Glu Ile Ala
 260 265 270
 Glu Ser His Arg Phe Cys Asp Gly Arg Val Gln Asp Ala Tyr Thr Leu
 275 280 285
 Arg Cys Cys Pro Gln Val His Gly Val Val Asn Asp Thr Ile Ala Phe
 290 295 300
 Val Lys Asp Ile Ile Thr Thr Glu Leu Asn Ser Ala Thr Asp Asn Pro
 305 310 315 320
 Met Val Phe Ala Ser Gly Glu Thr Ile Ser Gly Gly Asn Phe His Gly
 325 330 335
 Glu Tyr Pro Ala Lys Ala Leu Asp Tyr Leu Ala Ile Gly Val His Glu
 340 345 350
 Leu Ala Ala Ile Ser Glu Arg Arg Ile Glu Arg Leu Cys Asn Pro Ser
 355 360 365
 Leu Ser Arg Glu Leu Pro Ala Phe Leu Val Ala Glu Gly Gly Leu Asn
 370 375 380
 Ser Gly Phe Met Ile Ala His Cys Thr Ala Ala Ala Leu Val Ser Glu

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385		390		395		400									
Ser	Lys	Ala	Leu	Cys	His	Pro	Ser	Ser	Val	Asp	Ser	Leu	Ser	Thr	Ser
				405					410					415	
Ala	Ala	Thr	Glu	Asp	His	Val	Ser	Met	Gly	Gly	Trp	Ala	Ala	Arg	Lys
			420					425						430	
Ala	Leu	Arg	Val	Val	Glu	His	Val	Glu	Gln	Val	Leu	Ala	Ile	Glu	Leu
		435					440						445		
Leu	Ala	Ala	Cys	Gln	Gly	Ile	Glu	Phe	Leu	Arg	Pro	Leu	Lys	Thr	Thr
	450					455					460				
Thr	Pro	Leu	Glu	Lys	Val	Tyr	Asp	Leu	Val	Arg	Ser	Val	Val	Arg	Pro
465					470					475					480
Trp	Ile	Lys	Asp	Arg	Phe	Met	Ala	Pro	Asp	Ile	Glu	Ala	Ala	His	Arg
				485					490					495	
Leu	Leu	Leu	Asp	Gln	Lys	Val	Trp	Glu	Val	Ala	Ala	Pro	Tyr	Ile	Glu
			500					505						510	

Lys

<210> SEQ ID NO 61

<211> LENGTH: 513

<212> TYPE: PRT

<213> ORGANISM: Rattus sp.

<400> SEQUENCE: 61

Lys	Tyr	Arg	Glu	Pro	Glu	Lys	Tyr	Ile	Ala	Leu	Asp	Gly	Asp	Ser	Thr
1				5					10					15	
Glu	Asp	Leu	Val	Asn	Leu	Gly	Lys	Gly	His	Tyr	Lys	Ile	Lys	Leu	Thr
			20					25					30		
Ser	Ile	Ala	Glu	Lys	Lys	Val	Gln	Gln	Ser	Arg	Glu	Val	Ile	Asp	Ser
		35					40						45		
Ile	Ile	Lys	Glu	Arg	Thr	Val	Val	Tyr	Gly	Ile	Thr	Thr	Gly	Phe	Gly
	50					55					60				
Lys	Phe	Ala	Thr	Arg	Thr	Val	Ile	Pro	Ala	Asn	Lys	Leu	Gln	Leu	Gln
65					70					75					80
Val	Asn	Leu	Val	Arg	Ser	His	Ser	Ser	Gly	Val	Gly	Lys	Pro	Leu	Ser
				85					90					95	
Pro	Glu	Arg	Cys	Arg	Met	Leu	Leu	Ala	Leu	Arg	Ile	Asn	Val	Leu	Ala
			100					105					110		
Lys	Gly	Tyr	Ser	Gly	Ile	Ser	Leu	Glu	Thr	Leu	Lys	Gln	Val	Ile	Glu
		115					120					125			
Val	Phe	Asn	Ala	Ser	Cys	Leu	Ser	Tyr	Val	Pro	Glu	Lys	Gly	Thr	Val
	130					135					140				
Gly	Ala	Ser	Gly	Asp	Leu	Ala	Pro	Leu	Ser	His	Leu	Ala	Leu	Gly	Leu
145					150					155					160
Ile	Gly	Glu	Gly	Lys	Met	Trp	Ser	Pro	Lys	Ser	Gly	Trp	Ala	Asp	Ala
				165					170					175	
Lys	Tyr	Val	Leu	Glu	Ala	His	Gly	Leu	Lys	Pro	Ile	Val	Leu	Lys	Pro
		180						185					190		
Lys	Glu	Gly	Leu	Ala	Leu	Ile	Asn	Gly	Thr	Gln	Met	Ile	Thr	Ser	Leu
	195						200					205			
Gly	Cys	Glu	Ala	Val	Glu	Arg	Ala	Ser	Ala	Ile	Ala	Arg	Gln	Ala	Asp
	210					215					220				
Ile	Val	Ala	Ala	Leu	Thr	Leu	Glu	Val	Leu	Lys	Gly	Thr	Thr	Lys	Ala
225					230					235					240
Phe	Asp	Thr	Asp	Ile	His	Ala	Pro	Val	Arg	Pro	His	Arg	Gly	Gln	Ile

-continued

245				250				255							
Glu	Val	Ala	Phe	Arg	Phe	Arg	Ser	Leu	Leu	Ser	Asp	Ser	Glu	Ile	Ala
			260								265				270
Glu	Ser	His	Arg	Phe	Cys	Asp	Gly	Arg	Val	Gln	Asp	Ala	Tyr	Thr	Leu
		275					280					285			
Arg	Cys	Cys	Pro	Gln	Val	His	Gly	Val	Val	Asn	Asp	Thr	Ile	Ala	Phe
	290					295					300				
Val	Lys	Asp	Ile	Ile	Thr	Thr	Glu	Leu	Asn	Ser	Ala	Thr	Asp	Asn	Pro
305					310					315					320
Met	Val	Phe	Ala	Ser	Gly	Glu	Thr	Ile	Ser	Gly	Gly	Asn	Phe	His	Gly
			325							330				335	
Glu	Tyr	Pro	Ala	Lys	Ala	Leu	Asp	Tyr	Leu	Ala	Ile	Gly	Val	His	Glu
			340							345				350	
Leu	Ala	Ala	Ile	Ser	Glu	Arg	Arg	Ile	Glu	Arg	Leu	Cys	Asn	Pro	Ser
		355					360						365		
Leu	Ser	Arg	Glu	Leu	Pro	Ala	Phe	Leu	Val	Ala	Glu	Gly	Gly	Leu	Asn
	370					375					380				
Ser	Gly	Phe	Met	Ile	Ala	His	Cys	Thr	Ala	Ala	Ala	Leu	Val	Ser	Glu
385					390					395					400
Ser	Lys	Ala	Leu	Cys	His	Pro	Ser	Ser	Val	Asp	Ser	Leu	Ser	Thr	Ser
			405							410				415	
Ala	Ala	Thr	Glu	Asp	His	Val	Ser	Met	Gly	Gly	Trp	Ala	Ala	Arg	Lys
			420						425				430		
Ala	Leu	Arg	Val	Ile	Glu	His	Val	Glu	Gln	Val	Leu	Ala	Ile	Glu	Leu
		435					440						445		
Leu	Ala	Ala	Cys	Gln	Gly	Ile	Glu	Phe	Leu	Arg	Pro	Leu	Lys	Thr	Thr
	450					455					460				
Thr	Pro	Leu	Glu	Lys	Val	Tyr	Asp	Leu	Val	Arg	Ser	Val	Val	Arg	Pro
465					470					475					480
Trp	Ile	Lys	Asp	Arg	Phe	Met	Ala	Pro	Asp	Ile	Glu	Ala	Ala	His	Arg
			485						490					495	
Leu	Leu	Leu	Asp	Gln	Lys	Val	Trp	Glu	Val	Ala	Ala	Pro	Tyr	Ile	Glu
			500							505				510	

Lys

<210> SEQ ID NO 62
 <211> LENGTH: 513
 <212> TYPE: PRT
 <213> ORGANISM: Unknown Organism
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Unknown Organism: Uncultured
 bacterium pCosAS1

<400> SEQUENCE: 62

Met	Ala	Ser	Met	Asn	Ala	Leu	Thr	Leu	Thr	Pro	Gly	Thr	Leu	Thr	Leu
1				5					10					15	
Ala	Gln	Leu	Arg	Gln	Val	Trp	Gln	Gln	Pro	Leu	Gln	Leu	Thr	Leu	Asp
			20					25					30		
Glu	Ser	Ala	His	Glu	Ala	Ile	Asn	Asp	Ser	Val	Ala	Cys	Val	Glu	Ala
		35					40					45			
Ile	Val	Ala	Glu	Gly	Arg	Thr	Ala	Tyr	Gly	Ile	Asn	Thr	Gly	Phe	Gly
	50					55					60				
Leu	Leu	Ala	Gln	Thr	Arg	Ile	Ala	Thr	His	Asp	Leu	Glu	Asn	Leu	Gln
65					70					75					80
Arg	Ser	Leu	Val	Leu	Ser	His	Ala	Ala	Gly	Val	Gly	Glu	Pro	Leu	Asp

-continued

85					90					95					
Asp	Asp	Ile	Val	Arg	Leu	Met	Met	Val	Leu	Lys	Ile	Asn	Ser	Leu	Ala
			100					105					110		
Arg	Gly	Phe	Ser	Gly	Ile	Arg	Leu	Ser	Val	Ile	Gln	Ala	Leu	Ile	Ala
		115					120					125			
Leu	Val	Asn	Ala	Gly	Val	Tyr	Ser	Val	Asp	Pro	Ala	Lys	Gly	Ser	Val
	130					135					140				
Gly	Ala	Ser	Gly	Asp	Leu	Ala	Pro	Leu	Ala	His	Met	Ser	Leu	Thr	Leu
145					150					155					160
Leu	Gly	Glu	Gly	Lys	Ala	Arg	Asp	Tyr	Arg	Gly	Glu	Trp	Leu	Pro	Ala
				165					170					175	
Ala	Thr	Ala	Leu	Gln	Lys	Ala	Gly	Leu	Ala	Pro	Val	Thr	Leu	Ala	Ala
			180					185					190		
Lys	Glu	Gly	Leu	Ala	Leu	Leu	Asn	Gly	Thr	Gln	Ala	Ser	Thr	Ala	Phe
		195					200					205			
Ala	Leu	Arg	Gly	Leu	Phe	Glu	Ala	Glu	Asp	Leu	Phe	Ala	Ser	Ala	Val
	210					215					220				
Val	Cys	Gly	Ala	Leu	Thr	Thr	Glu	Ala	Val	Leu	Gly	Ser	Arg	Arg	Pro
225					230					235					240
Phe	Asp	Ala	Arg	Ile	His	Glu	Pro	Val	Arg	Gly	Gln	Arg	Gly	Gln	Ile
				245					250					255	
Asp	Ala	Ala	Ala	Leu	Phe	Arg	His	Val	Leu	Thr	Asp	Thr	Ser	Ala	Ile
			260					265					270		
Ala	Ser	His	His	Asn	Cys	Asp	Gly	Lys	Val	Gln	Asp	Pro	Tyr	Ser	Leu
		275					280					285			
Arg	Cys	Gln	Pro	Gln	Val	Met	Gly	Ala	Cys	Leu	Thr	Gln	Met	Arg	Gln
	290					295					300				
Val	Ala	Glu	Val	Leu	Leu	Val	Glu	Ser	Asn	Ala	Val	Ser	Asp	Asn	Pro
305					310					315					320
Leu	Val	Phe	Ala	Ala	Asn	Glu	Met	Val	Phe	Arg	Gly	Asn	Phe	His	Ala
				325					330					335	
Glu	Pro	Val	Ala	Met	Ala	Ala	Asp	Asn	Leu	Ala	Leu	Ala	Ile	Ala	Glu
			340					345					350		
Ile	Gly	Ala	Leu	Ser	Glu	Arg	Arg	Ile	Ala	Leu	Met	Met	Asp	Lys	His
		355					360					365			
Met	Ser	Gln	Asp	Leu	Pro	Pro	Phe	Leu	Val	Arg	Asn	Gly	Gly	Val	Asn
	370					375					380				
Ser	Gly	Phe	Met	Ile	Ala	Gln	Val	Thr	Ala	Ala	Ala	Leu	Ala	Ser	Glu
385					390					395					400
Asn	Lys	Gly	Leu	Cys	His	Pro	Thr	Ser	Val	Asp	Lys	Ile	Pro	Pro	Ser
				405					410				415		
Ala	Asn	Gln	Glu	Asp	His	Val	Ser	Met	Ala	Pro	Ala	Ala	Gly	Arg	Arg
			420					425					430		
Leu	Trp	Glu	Met	Ala	Gly	Asn	Thr	Arg	Gly	Val	Leu	Ala	Val	Glu	Trp
		435					440					445			
Leu	Ala	Ala	Cys	Gln	Gly	Ala	Asp	Leu	Arg	Asp	Gly	Leu	Thr	Ser	Ser
	450					455					460				
Pro	Leu	Leu	Glu	Gln	Ala	Arg	Gln	Ser	Cys	Gly	Glu	Gln	Val	Ala	His
465					470					475					480
Tyr	Asp	Asp	Asp	Arg	Phe	Phe	Ala	Pro	Asp	Ile	Glu	Ala	Ala	Ile	Ser
				485					490					495	
Leu	Leu	Asn	Lys	Gly	Ser	Leu	Val	Gly	Leu	Leu	Pro	Ala	Phe	Leu	Pro
			500					505					510		

-continued

Ala

<210> SEQ ID NO 63

<211> LENGTH: 513

<212> TYPE: PRT

<213> ORGANISM: Rhizobium meliloti

<400> SEQUENCE: 63

Met Ala Ser Ala Met Gly Glu Met Ile Ser Leu Asp Gly Pro Leu Thr
 1 5 10 15

Trp Arg Glu Ile Ala Ser Ile Ala Glu Gly Ala Ser Leu Asp Leu Ser
 20 25 30

Gly Pro Ala Arg Leu Arg Ile Ala Gln Ala Arg Arg Ile Val Asp Ala
 35 40 45

Leu Val Glu Arg Gly Ile Arg Gly Tyr Gly Ile Asn Thr Gly Val Gly
 50 55 60

Ala Leu Cys Asp Val Ile Ile Ser Arg Glu Asn Gln Gln Ala Leu Ser
 65 70 75 80

Arg Asn Ile Ile Leu Ser His Ala Cys Gly Val Gly Asp Pro Leu Gly
 85 90 95

Arg Val Glu Ala Arg Ala Val Met Ala Ala Gln Ile Ala Asn Leu Thr
 100 105 110

His Gly Tyr Ser Gly Val Arg Val Glu Thr Ala Glu Met Leu Leu Ala
 115 120 125

Leu Leu Asn Ala Asp Ile Ile Pro Leu Ile Pro Ser Arg Gly Ser Val
 130 135 140

Gly Tyr Ser Gly Asp Leu Ala Pro Leu Thr His Ala Ala Leu Val Leu
 145 150 155 160

Ile Gly His Gly Ser Ala Met Gln Gly Thr Glu Arg Leu Ser Gly Ala
 165 170 175

Asp Ala Leu Phe Ala Arg Leu Gly Leu Ala Pro Leu Arg Leu Glu Ala
 180 185 190

Lys Glu Gly Leu Ser Leu Val Asn Gly Thr Pro Cys Ala Thr Gly Leu
 195 200 205

Ala Ala Leu Ala Leu Ala Arg Thr Glu Arg Leu Phe Ala Trp Ala Asp
 210 215 220

Ala Ala Ala Ala Met Thr Tyr Glu Ala Asn Leu Gly Ser Gln Ala Asn
 225 230 235 240

Ala Phe Ala Glu Leu Pro Leu Ala Leu Arg Gln Ser Pro Gly Leu Ser
 245 250 255

Ala Val Gly Glu Gly Leu Arg Asp Trp Leu Ala Asp Ser Pro Met Leu
 260 265 270

Ala Gly His Arg Thr Ala Gly Thr Arg Thr Gln Asp Pro Leu Ser Leu
 275 280 285

Arg Ala Val Pro Gln Val His Gly Ala Ala Arg Asp Ala Phe Gly Gln
 290 295 300

Val Ala Glu Ile Val Asp Arg Glu Leu Ala Ser Val Thr Asp Asn Pro
 305 310 315 320

Ala Val Ala Gly Ser Pro Glu Val His Ser Gln Ala His Ala Val Gly
 325 330 335

Ala Ala Leu Gly Leu Ala Met Asp Ser Leu Ala Val Ala Val Ala Glu
 340 345 350

Val Ala Ala Ile Ser Glu Arg Arg Ile Asp Arg Leu Val Asn Pro Leu
 355 360 365

-continued

Val Ser Arg Gly Leu Pro Ala Phe Leu Ala Gly Asp Ser Gly Val Ser
 370 375 380

Ser Gly Phe Met Ile Ala Gln Tyr Thr Ala Ala Ala Leu Val Ala Glu
 385 390 395 400

Asn Arg Arg Leu Ala Ala Pro Ala Ser Leu Asp Gly Gly Ile Thr Ser
 405 410 415

Ala Leu Gln Glu Asp Met Leu Thr His Ala Thr Pro Ala Ala Trp Lys
 420 425 430

Ala Leu Ser Ile Val Asp Asn Leu Glu Arg Ile Leu Ala Ile Glu Leu
 435 440 445

Leu Ala Ala His Arg Pro Met Ser Cys Ser Arg Lys Arg Arg Ala Arg
 450 455 460

Arg Asn Ala Pro Leu Pro Phe Thr Gly Thr Tyr Ala Arg Arg Ser Pro
 465 470 475 480

Pro Ile Ala Thr Ile Val Arg Ser Ala Glu Leu Glu Ala Ala Tyr Asp
 485 490 495

Leu Leu Ala Asn Gly Ser Val His Lys Ala Leu Glu Ala His Leu Pro
 500 505 510

Ala

<210> SEQ ID NO 64
 <211> LENGTH: 513
 <212> TYPE: PRT
 <213> ORGANISM: Halobacterium sp.

<400> SEQUENCE: 64

Met Ala Ser Ala Pro Gln Ile Thr Leu Gly Leu Ser Gly Ala Thr Ala
 1 5 10 15

Asp Asp Val Ile Ala Val Ala Arg His Glu Ala Arg Ile Ser Ile Ser
 20 25 30

Pro Gln Val Leu Glu Glu Leu Ala Ser Val Arg Ala His Ile Asp Ala
 35 40 45

Leu Ala Ser Ala Asp Thr Pro Val Tyr Gly Ile Ser Thr Gly Phe Gly
 50 55 60

Ala Met Ser Asp Thr Arg Ile Asp Ala Ala Asp Arg Glu Ala Leu Gln
 65 70 75 80

Ala Asn Leu Val Arg Ser His Ala Ala Gly Ala Gly Ser Glu Leu Asp
 85 90 95

Thr Ala Ala Val Arg Ala Leu Leu Val Thr Arg Leu Asn Ala Leu Ala
 100 105 110

Lys Gly Tyr Ser Gly Ile Arg Glu Arg Val Leu Asp Val Leu Val Gly
 115 120 125

Leu Leu Asn Glu Gly Val His Pro Val Val Pro Ser Arg Gly Ser Leu
 130 135 140

Gly Ala Ser Gly Asp Leu Ala Pro Leu Ala His Met Ser Arg Val Leu
 145 150 155 160

Ile Gly Glu Gly Gln Ala Thr Asp Val Ala Gly Glu Arg Met Pro Ala
 165 170 175

Ala Glu Ala Leu Ala Ala Ala Asp Leu Glu Pro Val Thr Leu Gln Ala
 180 185 190

Lys Glu Gly Leu Ala Leu Ile Asn Gly Thr Gln Leu Thr Thr Gly Val
 195 200 205

Ala Ala Leu Ala Leu Val Asp Ala Glu Arg Val Leu Arg Ser Ala Asp
 210 215 220

-continued

Thr Ala Gly Ala Leu Thr Thr Glu Val Thr Met Ser Thr Thr Ala Ser
 225 230 235 240
 Cys Ala Pro Ala Ile His Glu Pro Val Arg Pro His Asp Gly Gln Ala
 245 250 255
 Val Ser Ala Arg His Ile Arg Asn Leu Thr Ala Gly Ser Glu Val Leu
 260 265 270
 Asp His His Arg Asp Cys Asp Gly Arg Val Gln Asp Ala Tyr Ser Ile
 275 280 285
 Arg Cys Leu Pro Gln Val His Gly Ala Val Arg Asp Ala Leu Asp His
 290 295 300
 Leu Arg Ala Ala Val Ala Thr Glu Leu Asn Ser Ala Thr Asp Asn Pro
 305 310 315 320
 Leu Val Phe Pro Ser Gly Thr Val Val Ser Gly Gly Asn Phe His Gly
 325 330 335
 Glu Val Leu Ala Leu Arg Leu Gly Tyr Ala Ala Ser Ala Leu Ala Glu
 340 345 350
 Leu Ala Ala Ile Ser Glu Arg Arg Thr Asp Arg Leu Leu Asn Pro Glu
 355 360 365
 Thr Gln Glu Pro Leu Glu Pro Phe Leu Ala Pro Asp Ser Gly Leu His
 370 375 380
 Ser Gly Leu Met Ile Pro Gln Tyr Thr Ala Ala Ser Leu Val Asn Asp
 385 390 395 400
 Leu Arg Ser Leu Gly Gln Pro Ala Thr Leu Asp Asn Ala Ser Val Ser
 405 410 415
 Gly Ala Gln Glu Asp His Val Ser Met Ser Ala Gly Ala Ala Tyr Asn
 420 425 430
 Phe Arg Glu Ala Val Glu Lys Ala Ala Thr Val Val Gly Val Glu Leu
 435 440 445
 Leu Cys Gly Ala Gln Gly Arg Glu Phe Leu Asp Pro Leu Ala Leu Gly
 450 455 460
 Ala Gly Thr Ala Ala Ala Tyr Asp Leu Val Arg Ser Glu Val Ser Glu
 465 470 475 480
 Pro Ala Gly Asp Arg Ala Leu Ala Asp Asp Met Ala Ala Val Gly Asp
 485 490 495
 Leu Val Arg Ala Gly Leu Val Glu Asp Ala Val Ala Arg Ala Leu Asp
 500 505 510

Ala

<210> SEQ ID NO 65
 <211> LENGTH: 504
 <212> TYPE: PRT
 <213> ORGANISM: Streptomyces griseus

<400> SEQUENCE: 65

Val Val Val Gly Thr Ser Gly Thr Thr Ala Glu Asp Val Val Ala Val
 1 5 10 15
 Ala Arg His Gly Ala Arg Val Glu Leu Ser Ala Ala Ala Val Glu Ala
 20 25 30
 Leu Ala Ala Ala Arg Leu Ile Val Asp Ala Leu Ala Ala Lys Pro Glu
 35 40 45
 Pro Val Tyr Gly Val Ser Thr Gly Phe Gly Ala Leu Ala Ser Arg His
 50 55 60
 Ile Gly Thr Glu Leu Arg Ala Gln Leu Gln Arg Asn Ile Val Arg Ser
 65 70 75 80

-continued

His Ala Ala Gly Met Gly Pro Arg Val Glu Arg Glu Val Val Arg Ala
 85 90 95

Leu Met Phe Leu Arg Leu Lys Thr Val Ala Ser Gly His Thr Gly Val
 100 105 110

Arg Pro Glu Val Ala Gln Thr Met Ala Asp Val Leu Asn Ala Gly Ile
 115 120 125

Thr Pro Val Val His Glu Tyr Gly Ser Leu Gly Cys Ser Gly Asp Leu
 130 135 140

Ala Pro Leu Ser His Cys Ala Leu Thr Leu Met Gly Glu Gly Glu Ala
 145 150 155 160

Glu Gly Pro Asp Gly Thr Val Arg Pro Ala Gly Glu Leu Leu Ala Ala
 165 170 175

His Gly Ile Ala Pro Val Glu Leu Arg Glu Lys Glu Gly Leu Ala Leu
 180 185 190

Leu Asn Gly Thr Asp Gly Met Leu Gly Met Leu Val Met Ala Leu Ala
 195 200 205

Asp Leu Arg Asn Leu Tyr Thr Ser Ala Asp Ile Thr Ala Ala Leu Ser
 210 215 220

Leu Glu Ala Leu Leu Gly Thr Asp Lys Val Leu Ala Pro Glu Leu His
 225 230 235 240

Ala Ile Arg Pro His Pro Gly Gln Gly Val Ser Ala Asp Asn Met Ser
 245 250 255

Arg Val Leu Ala Gly Ser Gly Leu Thr Gly His His Gln Asp Asp Ala
 260 265 270

Pro Arg Val Gln Asp Ala Tyr Ser Val Arg Cys Ala Pro Gln Val Asn
 275 280 285

Gly Ala Gly Arg Asp Thr Leu Asp His Ala Ala Leu Val Ala Gly Arg
 290 295 300

Glu Leu Ala Ser Ser Val Asp Asn Pro Val Val Leu Pro Asp Gly Arg
 305 310 315 320

Val Glu Ser Asn Gly Asn Phe His Gly Ala Pro Val Ala Tyr Val Leu
 325 330 335

Asp Phe Leu Ala Ile Val Ala Ala Asp Leu Gly Ser Ile Cys Glu Arg
 340 345 350

Arg Thr Asp Arg Leu Leu Asp Lys Asn Arg Ser His Gly Leu Pro Pro
 355 360 365

Phe Leu Ala Asp Asp Ala Gly Val Asp Ser Gly Leu Met Ile Ala Gln
 370 375 380

Tyr Thr Gln Ala Ala Leu Val Ser Glu Met Lys Arg Leu Ala Val Pro
 385 390 395 400

Ala Ser Ala Asp Ser Ile Pro Ser Ser Ala Met Gln Glu Asp His Val
 405 410 415

Ser Met Gly Trp Ser Ala Ala Arg Lys Leu Arg Thr Ala Val Asp Asn
 420 425 430

Leu Ala Arg Ile Val Ala Val Glu Leu Tyr Ala Ala Thr Arg Ala Ile
 435 440 445

Glu Leu Arg Ala Ala Glu Gly Leu Thr Pro Ala Pro Ala Ser Glu Ala
 450 455 460

Val Val Ala Ala Leu Arg Ala Ala Gly Ala Glu Gly Pro Gly Pro Asp
 465 470 475 480

Arg Phe Leu Ala Pro Asp Leu Ala Ala Ala Asp Thr Phe Val Arg Glu
 485 490 495

-continued

Gly Arg Leu Val Ala Ala Val Glu
500

<210> SEQ ID NO 66
<211> LENGTH: 502
<212> TYPE: PRT
<213> ORGANISM: Corynebacteriaceae sp.

<400> SEQUENCE: 66

Ile Thr Leu Gly Leu Ser Gly Ala Thr Ala Asp Asp Val Ile Ala Val
1 5 10 15
Ala Arg His Glu Ala Arg Ile Ser Ile Ser Pro Gln Val Leu Glu Glu
20 25 30
Leu Ala Ser Val Arg Ala His Ile Asp Ala Leu Ala Ser Ala Asp Thr
35 40 45
Pro Val Tyr Gly Ile Ser Thr Gly Phe Gly Ala Leu Ala Thr Arg His
50 55 60
Ile Ala Pro Glu Asp Arg Ala Lys Leu Gln Arg Ser Leu Ile Arg Ser
65 70 75 80
His Ala Ala Gly Met Gly Glu Pro Val Glu Arg Glu Val Val Arg Ala
85 90 95
Leu Met Phe Leu Arg Ala Lys Thr Leu Ala Ser Gly Arg Thr Gly Val
100 105 110
Arg Pro Val Val Leu Glu Thr Met Val Gly Met Leu Asn Ala Gly Ile
115 120 125
Thr Pro Val Val Arg Glu Tyr Gly Ser Leu Gly Cys Ser Gly Asp Leu
130 135 140
Ala Pro Leu Ser His Cys Ala Leu Val Leu Met Gly Glu Gly Glu Ala
145 150 155 160
Thr Asp Ala His Gly Asp Ile Arg Pro Val Pro Glu Leu Phe Ala Glu
165 170 175
Ala Gly Leu Thr Pro Val Glu Leu Ala Glu Lys Glu Gly Leu Ala Leu
180 185 190
Val Asn Gly Thr Asp Gly Met Leu Gly Gln Leu Ile Met Ala Leu Ala
195 200 205
Asp Leu Asp Glu Leu Leu Asp Ile Ala Asp Ala Thr Ala Ala Met Ser
210 215 220
Val Glu Ala Gln Leu Gly Thr Asp Gln Val Phe Arg Ala Glu Leu His
225 230 235 240
Glu Pro Leu Arg Pro His Pro Gly Gln Gly Arg Ser Ala Gln Asn Met
245 250 255
Phe Ala Phe Leu Ala Asp Ser Pro Ile Val Ala Ser His Arg Glu Gly
260 265 270
Asp Gly Arg Val Gln Asp Ala Tyr Ser Leu Arg Cys Ser Pro Gln Val
275 280 285
Thr Gly Ala Ala Arg Asp Thr Ile Ala His Ala Arg Leu Val Ala Thr
290 295 300
Arg Glu Leu Ala Ala Ala Ile Asp Asn Pro Val Val Leu Pro Ser Gly
305 310 315 320
Glu Val Thr Ser Asn Gly Asn Phe His Gly Ala Pro Val Ala Tyr Val
325 330 335
Leu Asp Phe Leu Ala Ile Ala Val Ala Asp Leu Gly Ser Ile Ala Glu
340 345 350
Arg Arg Thr Asp Arg Met Leu Asp Pro Ala Arg Ser Arg Asp Leu Pro
355 360 365

-continued

Ala	Phe	Leu	Ala	Asp	Asp	Pro	Gly	Val	Asp	Ser	Gly	Met	Met	Ile	Ala
	370					375					380				
Gln	Tyr	Thr	Gln	Ala	Gly	Leu	Val	Ala	Glu	Asn	Lys	Arg	Leu	Ala	Val
385					390					395					400
Pro	Ala	Ser	Val	Asp	Ser	Ile	Pro	Ser	Ser	Ala	Met	Gln	Glu	Asp	His
				405					410					415	
Val	Ser	Leu	Gly	Trp	His	Ala	Ala	Arg	Lys	Leu	Arg	Thr	Ser	Val	Ala
			420					425					430		
Asn	Leu	Arg	Arg	Ile	Leu	Ala	Val	Glu	Met	Leu	Ile	Ala	Gly	Arg	Ala
		435					440						445		
Leu	Asp	Leu	Arg	Ala	Pro	Leu	Lys	Pro	Gly	Pro	Ala	Thr	Gly	Ala	Val
	450					455					460				
Leu	Glu	Val	Leu	Arg	Ser	Lys	Val	Ala	Gly	Pro	Gly	Gln	Asp	Arg	Phe
465					470					475					480
Leu	Ser	Ala	Glu	Leu	Glu	Ala	Ala	Tyr	Asp	Leu	Leu	Ala	Asn	Gly	Ser
				485					490					495	
Val	His	Lys	Ala	Leu	Glu										
				500											

What is claimed is:

1. A method of treating a viral infection, comprising administering to a patient suffering from the viral infection a therapeutic amount of a polypeptide having histidine ammonia lyase activity.

2. The method according to claim 1, wherein the histidine ammonia lyase activity is about 40 IU/mg protein and the polypeptide corresponds in sequence to histidine ammonia lyase of Corynebacteriaceae.

3. The method according to claim 1, wherein the histidine ammonia lyase activity is not substantially decreased in the presence of L-histidinol or a therapeutic salt thereof.

4. The method according to claim 3, further comprising administering a therapeutic amount of L-histidinol or a therapeutic salt thereof.

5. The method according to claim 1, wherein the viral infection is caused by a virus is selected from the group consisting of Herpes Virus Type 1, Herpes Simplex Virus Type 2, Varicella-Zoster Virus, Epstein-Barr virus, Cytomegalovirus, Respiratory Syncytial Virus, and Human Immunodeficiency Virus.

6. The method according to claim 1, wherein the polypeptide is selected from the group consisting of SEQ ID NOS: 1-5, 8-10, and 12.

7. The method according to claim 1, wherein the polypeptide comprises conservative substitutions relative to the sequence of histidine ammonia lyase of Corynebacteriaceae and wherein the polypeptide maintains the histidine ammonia lyase activity.

8. The method according to claim 7, wherein the polypeptide comprises SEQ ID NOS: 6 or 11, wherein each amino acid represented by an "X" is substituted with an amino acid from the corresponding position of the histidine ammonia lyase selected from the group consisting of Corynebacteriaceae, *Streptomyces coelicolor*, *Agrobacterium rhizogenes*, *Vibrio cholerae*, *Pseudomonas aeruginosa*, *Bacillus halodurans*, *Pseudomonas aeruginosa*, *Thermoplasma acidophilum*, *Mus musculus*, rat, uncultured bacterium pCosAS1, *Rhizobium meiloti*, and *Halobacterium* sp and wherein at least one of the amino acids represented by an "X" is not substituted with an amino acid from the

corresponding position of the histidine ammonia lyase of Corynebacteriaceae.

9. A method for treating a patient suffering from a cancer, comprising administering to the patient suffering from said cancer a therapeutic amount of a polypeptide having about 40 IU/mg protein of histidine ammonia lyase activity, wherein said histidine ammonia lyase activity is not substantially decreased in the presence of L-histidinol or a therapeutic salt thereof and the polypeptide corresponds in sequence to histidine ammonia lyase of Corynebacteriaceae, and a therapeutic amount of L-histidinol or a therapeutic salt thereof.

10. The method according to claim 9, wherein the polypeptide is selected from the group consisting of SEQ ID NOS: 1-5, 8-10, and 12.

11. The method according to claim 9, wherein the polypeptide comprises conservative substitutions relative to the sequence of histidine ammonia lyase of Corynebacteriaceae and wherein the polypeptide maintains the histidine ammonia lyase activity.

12. The method according to claim 11, wherein the polypeptide comprises SEQ ID NOS: 6 or 11, wherein each amino acid represented by an "X" is substituted with an amino acid from the corresponding position of the histidine ammonia lyase selected consisting of Corynebacteriaceae, *Streptomyces coelicolor*, *Agrobacterium rhizogenes*, *Vibrio cholerae*, *Pseudomonas aeruginosa*, *Bacillus halodurans*, *Pseudomonas aeruginosa*, *Thermoplasma acidophilum*, *Mus musculus*, rat, uncultured bacterium pCosAS1, *Rhizobium meiloti*, and *Halobacterium* sp and wherein at least one of the amino acids represented by an "X" is not substituted with an amino acid from the corresponding position of the histidine ammonia lyase of Corynebacteriaceae.

13. A method for reducing toxicity to normal cells from chemotherapeutic agents, comprising

- (i) administering to a patient a therapeutically effective amount of a polypeptide having histidine ammonia lyase activity, and
- (ii) additionally administering to said patient a therapeutically effective amount of a chemotherapeutic agent,

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whereby said polypeptide having histidine ammonia lyase activity selectively depletes circulating histidine and causes growth arrest in normal cells, without affecting the growth of tumor cells.

14. The method according to claim **13**, wherein upon the administration of said polypeptide, non-diseased cells of said patient enter a reversible quiescent state.

15. The method according to claim **13**, wherein the polypeptide is a modified polypeptide that comprises polyethylene glycol.

16. A method for delivering an immunosuppressant to a patient, comprising: administering to a patient a therapeutically effective amount of a polypeptide having histidine ammonia lyase activity, wherein said polypeptide is PEGylated and wherein said polypeptide generates trans-urocanic acid (t-UA) in vivo; and subjecting the patient to an irradiating agent, wherein said irradiating agent causes the photo-

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toisomerization of t-UA to its cis isomer (c-UA), and wherein said cis isomer comprises an immunosuppressive property.

17. The method according to claim **16**, wherein the irradiating agent is UVB irradiation, and wherein the polypeptide comprises polyethylene glycol.

18. The method according to claim **17**, wherein the patient has an immune system disorder.

19. The method according to claim **18**, wherein the UVB radiation is localized.

20. The method according to claim **16**, further comprising administering to the patient a transplanted organ.

21. A method of treating a viral infection comprising administering to a patient suffering from the viral infection a therapeutic amount of a histidine analog and a polypeptide having histidine ammonia lyase activity.

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